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(51) International Patent Classification ⁶ : C12Q 1/68	A2	(11) International Publication Number: WO 98/20165 (43) International Publication Date: 14 May 1998 (14.05.98)
<p>(21) International Application Number: PCT/US97/20313</p> <p>(22) International Filing Date: 5 November 1997 (05.11.97)</p> <p>(30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US</p> <p>(71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US/US); Nine Cambridge Center, Cambridge, MA 02142 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. (US/US); 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David (CN/US); Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas (CA/US); 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).</p> <p>(74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).</p>		<p>(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).</p> <p>Published Without international search report and to be republished upon receipt of that report.</p>
<p>(54) Title: BIALLELIC MARKERS</p> <p>(57) Abstract</p> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

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As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

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30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

15 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

25 Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally PCR Technology:
10 *Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson
15 et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

- 5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
- 10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
- 15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
- 20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

- The direct analysis of the sequence of polymorphisms of
- 25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
- 30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with
polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- 15 The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- 20 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- 30 The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTCT GAAACCTCAGTGCATAATAGGAACACTTGGAGACTAATGAAGAGAGAGATTGAGACCAATCTTTATTT GTACTGGCCAAATACCTAAACAGTTGAAGGAAGACATTTGGAAGAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTCTTTTC/TTAGTTTAAATGCTGTCTCTGTCTGAG
WI-7070	226	C	T	---	---	AAAGCCATTGACGTACATCTCAGAGGTTATTTGCAATGGATTGACTCTCTGGGACAAAAGGAC(G/C)AA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCTAGGATTTAGATACAACTCTTGAAGAAAGAACTGAGACAGATAATCTGAATT AAATGAGGTAAGTTTCAGGCCTCA
WI-10744	61	G	C	---	---	GGGCAAAATACCAGCAAAAAGTCAAAATACACAGCATCAAGTCAGGTGC AAAAGGAGGTAGAACAA TTACAGTAACATATGTCAATCTTTTGTATTATTAGTATTATCTGCCCAATGCCCTAGATAIC/TTAGTG GGTCCCTAATAGTTATAGTTCCTTTTCTCCCTCTCTCTCAITCTCTGAATTTATTTTATACTTAA GGGATTAGTACCACCAAAATGTATGTATCAAAATTTGATCTTACTGAA
WI-9975	126	C	T	---	---	GCTAGGTTTTGTTCTGTGGCTGTCTTCACTAGACTTGAGATGACTTGAATTTACAGTAATCCCTATGT GATGTAACATGCTAGACCTCCCTTCGCCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCTCTCTCCAGTTTCTCCTGTATTAATTTCTCCCATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAGAAATAAAGAGATCCCAAGTGGTGGGG(G/T)CTT
WI-8010	247	G	T	---	---	GCCGGCCTATCTTTTAAATTTAACTTGATCTTTGGTGTTCTCCATCCTAGGATCTGSCCTTATAAT CTTTGTCTGTCTGTAG/GC/ATTACCTGATCTACTTTTGTATACACAGGCTGATGGCTCACAATGT AGTAGTCCCAATCTTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTCTACTTA TCTCGACTCTATAACAACTCCACAGAA
WI-5222b	85	G	C	---	---	GCCGGCCTATCTTTTAAATTTAACTTGATCTTTGGTGTTCTCCATCCTAGGATCTGSCCTTAT AATCTTGTCTGTCTGTAGATTACCTGATCTACTTTTGTATACACAGGCTGATGGCTCACAATGT AGTAGTGC AATCTTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTCTACTTA TCTCGACTCTATAACAACTCCACAGAA
WI-5222	52	G	C	---	---	TATGCATCTCCACAAAAGCGATATAATTTAAAGTTTTTTCATTAGAAATAAATGTATAAAATAA ATATGTTATTATAGGCATTTTACTAATCTAGTCTCTTGGGAAGGAACACCCCAACCAATACTT ATAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACGAGTACGACTGTTGGAC(G/A)AGCTGCTG
WI-8007	242	C	A	---	---	TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTCATATGTATGTTTGTAG TCTATATTCACACATATGAGTGAATTTCTGTTGGGCAATGGGAAATACATCTTTATGAGACATTTGA ACTGCTCACCACATCATAGTATCCATTTTAAACAGACACCAACATGTATAAGAAATCCCTTTGTTTAC ATGCTTTCCAAATCTGATTTTGTATGACTATTGTATGACACAGTTGGATCACC
WI-9823	97	C	T	---	---	

WI-9651b	105 A T	---	---	---	TCCTACATTCATGGCAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGAATTCCTTTCCCT ACTTGTCTCATGTACAAATTTTCTGCTGCTCTCAATJGGGCGAGCTTGCAGGCTCCCTTTAGAC ACCTCAGAGGTACAGCGACCACTGCCCTACTCCATGCGACTGCCAGGAGCCCTTATAGGCTCTG TCCTTAAACCTGTATGGTATATTAACTCTGGTGTGAATGCTCTC
WI-9651	139 T C	---	---	---	TCCTACATTCATGGCAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGAATTCCTTTCCCT ACTTGTCTCATGTACAAATTTTCTGCTGCTCTCAAGGGCAGCTTGCAGGCTCCCTTTAGACACCT CTGACAGGTACAGCGACCACTGCCCTACTCCATGCGACTGCCAGGAGCCCTTATAGGCTCTGT CTTTAAACCTGTATGGTATATTAACTCTGGTGTGAATGCTCTC
WI-7676b	309 A C	---	---	---	GTGACCTTCCTGCGAGGTGAGATGGACATCCTTCTGCTGCGGAGCTTGGCCCTGCTATTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCTCCAAAGGTAGATGGGAGGCTCTGTGTGAAGGG GCGGTCTCTGTGGCTCTGGGTTGCAGGGCAGGAGCGGTGGAGCTGCGACTTCTGCTGCTGCTG TCCCGGCTCTCTGCGAGGAGTATAGGAGAGAGCAAGGATTGAT
WI-7676	139 C T	---	---	---	GTGACCTTCCTGCGAGGTGAGATGGACATCCTTCTGCTGCGGAGCTTGGCCCTGCTATTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCTCCAAAGGTAGATGGGAGGCTCTGTGTGAAGGG GCGGTCTCTGTGGCTCTGGGTTGCAGGGCAGGAGCGGTGGAGCTGCGACTTCTGCTGCTGCTG GTGCTCCCGGCTCTCTGCGAGGAGTATAGGAGAGAGCAAGGATT
WI-10072	105 G A	---	---	---	CATATCTGTCTCTGGGCTGTTCATTCACCTTTCTCTCTCCAATGAAGAGGATATTAAAGCATCAT CATCTGGCCCTTTTGTAGTTTTGAATATTTTGTG/AJTGACTCTCTATGCACATGATAAATTTGTTA TGCTTGTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATAGAGGAGAAAGGGA TCACCCCTTTTTGCCTACAACTTATAGATATTAAATATCTTT
WI-9986	42 T C	---	A	---	TGGTGTGAACCTCAGAATATAGGAAATAAGACAAATTTGAAT/A CJGTACCCAGGAACAAGAG CCCTGCACCTTGACCTCAAAAGGTTCTATCTATCTGGCTGTTCCGAGACTTATTGTATCTTGAA GAGAACTTTTCCCTTAATCAGTTCTATCTGTATCCAGGCTAGTACTCACAAAGACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATGCAATT
WI-7041	174 C A	---	---	---	GTCTATTGAGGAGAAAGTCCCTTGGCACTCCCACTCTCATAGCCCAAGTGGAGGACTGGCCAGA GGGCTGCAATGCAACTCAGTCCCTGCTTTCAGAGAGCTGAAAGGGTCCCTCGGCTTTTATTT CAGGGCTTTGCATGCGCTCTATTCCCGCTCTGCTCTC/AJCCACTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCAATTGTACAGTGCTCTGTTCATGTAATAA
WI-7224	124 T C	---	---	---	ATAACCCCTTGTGTATGTATCAACCACTCACTAATATCAACTTATGTGCTATCAGATATCCCTCT ACCTCAGGTTATTTGAAGAAATCCTAAACATCAAACTTTCATGCTATCCATAAAATGTCAGCATTT /CJATTAAAAAATAAGCTTTTAAAGAAACATTAAGGACACATTTTCAAATTAATAAAATAAG GCATTTTAAAGGATGGCCTGTGATATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C	TCTATTGCAATTCACAGTAGCCCCATGAAGTAGGTATACAGCCCTCTATTTAATGAGAAGAT GGAGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAAGCAAGACCTGCAJAC JCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGAGCGAGGCCATCGGCA GAAAGCCAGCCCTCTCCATCCCCAC
TGR- A004S25	145 G A	AGATCTGCCATTAGTAATTTATCTTTGAAGTACTTTGGAGATTCAITTTCTGAGTGGCACTGCAT GCTCATTCAGTGAAGAACTTTGGGGTAGAAAATGGAAATGGAGATTTCAACAGCTTTGCTGAAAC TGACTTTGGGAGJCTCCAGACTTCACTGTCTTAGGCAITTGAAACCATCACCTGGTTTGCATCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T	AAACACAGAAATCATCAAGGACATATCTGTGTTTGAGATAAATGATAGTCTGAGTCACTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATATCAATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTTCTATGGAACTCTCCGTACTGTAAATTTTCAATCTATGGAACCTCCCATACTGT AATGGACAGTTTGGTTCCAC
WI-4687	121 G T	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATGAAGACACTTTTGAATGGTCTTGTCC TTTCAATAAAGAGGTGACATGATTGAACATGTGTTTATAGATAAGGGCACTTIGTJGAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAGGAAGATCAGGAAGAAAGTAGGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTAATGGGCTAGTCTTTGGGTGTGAGCGGATT ATGATCTGACGCCATGGGTGTTCAATAGTGACTTGAGAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTTGTTATTCATTCACAAATCTCTGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTCCACTTGTCAACTTATCTTAAGACATTTTTCACAGGA
WI-4719	70 G A	TTCAACACGCTTTATGGCACCTTGGCTCCCTCTGCCAGCAAGATCTTACCTCTTACCCCTGTAGG AATAGTACGCTCCGATGCCAGGGGAATGGGTGGGGTGTACCACTTCTCTCTGCACACTGCCAAGT TAAAGAAACCCCTTGTCTGGAGGGAGGCGGACAGAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCTGGJACTGACAGATATAGGACCAAGGGTTCCAACTTT
WI-9484b	216 G C	TCAACACGCTTTATGGCACCTTGGCTCCCTCTGCCAGCAAGATCTTACCTCTTACCCCTGTAGG AATAGTACGCTCCGATGCCAGGGGAATGGGTGGGGTGTACCACTTCTCTCTGCACACTGCCAAGT TAAAGAAACCCCTTGTCTGGAGGGAGGCGGACAGAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCTGGJACTGACAGATATAGGACCAAGGGTTCCAACTTT
WI-9484	178 G A	TCAACACGCTTTATGGCACCTTGGCTCCCTCTGCCAGCAAGATCTTACCTCTTACCCCTGTAGG AATAGTACGCTCCGATGCCAGGGGAATGGGTGGGGTGTACCACTTCTCTCTGCACACTGCCAAGT TAAAGAAACCCCTTGTCTGGAGGGAGGCGGACAGAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCTGGJACTGACAGATATAGGACCAAGGGTTCCAACTTT

[illegible]

WI-931c	191 C A	---	---	GACAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCTTCT GTTGCTGCACTGCTATTCTGTTGATGGATTATTAATTGTCCAAAAAGCC/CACGAGCCCTGG TACAGAAAGGCAATGGGAAAGATGTGCAGA
WI-931b	81 A G	---	---	GACAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTTACGTTCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCTGTTGCTGCACTGCTATTCTGTTGATGGATTATTAATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCAATGGGAAAGATGTGCAGA
WI-931	31 A G	---	---	GACAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAAACCTTGACACCCCTGGAGTT GTTTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCTGTTGCTGCACTGCTATTCTGTTGATGGATTATTAATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCAATGGGAAAGATGTGCAGA
WI-10870b	91 C T	---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGAGTGGCAGA GATCCACCTTAGCAAGTGGG/CACCTACTTAGCAGCAGTGGAGTACCCCTGAGTACGACCCCT TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAATAGGACATGGGTACGC CTGAGCCACTCTTAACCATGAACCATCACCATTAAATAACGTTGCCCCCTCC
WI-10870	103 G A	---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGAGTGGCAGA GATCCACCTTAGCAAGTGGGACACCTACTTAGAG/CAGTGGAGTACCCCTGAGTACGACCCCT TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAATAGGACATGGGTACGC CTGAGCCACTCTTAACCATGAACCATCACCATTAAATAACGTTGCCCCCTCC
WI-7719b	281 T C	---	---	AGTTTATCTCCAGATGACAGCAGTAGACAATGGATAGTACGAGAGTCTTAGGTAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAGTCTACAATGCCAATATCAAGCACAACCCCTAGC TCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGACCAATATGTG ATTCTGGACATTGCCCATGTATAATCTCCTCAGTGAATTCAGCTAAAGCAA
WI-7719	163 A G	---	---	AGTTTATCTCCAGATGACAGCAGTAGACAATGGATAGTACGAGAGTCTTAGGTAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAGTCTACAATGCCAATATCAAGCACAACCCCTAGC TCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGACCAATAT GTGATTTCTGGACATTGCCCATGTATAATCTCCTCAGTGAATTCAGCTAAAGCAA
WI-10396	72 C A	---	---	GCTTGGAGTATATCTAACTGTGGCTCCACTTCTTTCTTGAACATTGCTATCACTGGGAA GAGT/CAGTGTGACITTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTCTTTTGA TGCCATTGAGGGGATGTGTTTCTTAACTATGAAGTACTTGGCTGTCTCTCCCTGCTGTTGAGG TTAACAGCCACATTGTAAACACTTGT

WI-10673	94 C G ...			TCCTTTATGACCCCAAGAGATATTTATTAACACCAATTAAGTAGCAGGCCATGGCTCATGGGAAC CACCCCGGTGGCACTATGAGGGGGGCTGACAGTTGGAACTATGCAAGTGTCTCGGCCACACA TCCTGCTGGGCCCCCTACCCCTGCCCAATTAATCCTGCTTAATTTGTTTCATCTG GAGAAATTGAAGGGAGGTCAAGTTGTTGTCATGATTTGTCAGAGAACCCT
WI-7842	57 T C ...			CACAGCATGCCCTTGAGGAGCGGCCACACAGATGCTGAATCCCTATCCCATTTCTGTCGTATGAG TCCCATTTGCCCTTGCAATTAGCATTTCTGTCGCCCAAAAAGAAATGTCTATGAAGCTTTCTTCCT ACACACTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACAGAGCTAGTTTTCAGCTGCTCAGAA TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ...			CTGCTCATCAGCCCACTGGAGTCCACACTTGAATTTTGGGCACTACACGGGTCTGCCATGCTCTGG AGGAGAAAGGGGGCCACATCCCAACCCAGCTGTACCCAGCCCGGGCAGGTGCAGCCCTTCTCTCC TGTCTCTGCTGCTGCTCTCTTTTGGAGTCCCTGTATGTCCTACCTCTGACTTCTGTGTCCTCTG TGTCTCTCTCATCATCTCTCTACTGGGGCTGGGGCTCTAGCCAA
WI-4767b	173 C A ...			TTTCCAGTCTGTTTATCCTTTTATGCTCAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCT CAGGTCTGGTAACTCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTT CTTCCCTTGAGAAATCCTAGAAAGCACAGGGATGACAC/A/AAATCACTAAGGAATTCCTACTAAGA CTCCTTAACCCAGAGATTTTAACT
WI-4767	50 A G ...			TTTCCAGTCTGTTTATCCTTTTATGCTCAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTT CCTCAGGTCTGGTAACTCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTTCTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTTAACCCAGAGATTTTAACT
WI-7718f	222 C T ...			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGT ACTTTGCAGATGGAAGAGGTGAAATGAAGAAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATACAAAGAA/C/T/CATGCAAGGAAGGAAAACTATGTATTAA
WI-7718e	60 T C ...			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTCGAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA
WI-7718d	31 G A ...			ATTGCACTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTCGAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA

WI-7718c	91 C G	ATTGCACCTGAAGTTTTGAAATACCTTTGTAGTTACTAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGGTGAGTGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAT
WI-7718b	248 A G	ATTGCACCTGAAGTTTTGAAATACCTTTGTAGTTACTAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGGTGAGTGTTCACTACATGTTCTGGGGCCCGGAGATAG ACTTGCAGATGGAAGAGGTGAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTATGAT
WI-7718a	42 A T	ATTGCACCTGAAGTTTTGAAATACCTTTGTAGTTACTAAGCAGTTACTCCCTACACTGATG AAGGATTACAGAACTGATGCCAAGGGGCGGTGAGTGTTCACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAT
WI-7227d	99 G C	AGGGAATTGTTGCTCTCGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTACAGACAACTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTCGCTTTCAACCCAGCGACTAATGCAAT
WI-7227c	291 G A	AGGGAATTGTTGCTCTCGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTACAGACAACTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTAGTATCTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTCGCTTTCAACCCAGCGACTAATGCAAT
WI-7227b	93 G T	AGGGAATTGTTGCTCTCGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTACAGACAACTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTCGCTTTCAACCCAGCGACTAATG
WI-7227a	24 A G	AGGGAATTGTTGCTCTCGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCATCTTTACAGACAACTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTCGCTTTCAACCCAGCGACTAATG
WI-7310b	234 A/C	CCACAATGCTCTCCACGATGCAAGGACTCTGCTGCTCGAGGTGGGAGACAAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGATCCTTCAGAACAAAGTGTGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTCTATTGAACTGAGCCCAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCATCCCAACATGATGATCTGAGATTTC

WI-7310a	64	T A	CCACAATGCCCTCCACGATGCAAGGACTCCTGTCGTCTGGAGGTGGAGACAAAGAACCTTAA JCCGAAGAGGAGCAAGAAAGCCGTACTGTCTATGTTGATCCTTCATCGAACAAACTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCCATCCCAAATGATCTTGAGATTTC
WI-7878b	162	A G	CCAGCAACACCTACACCTTGTCACTGCCCTGGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCCAAGAGCGGCTCCTGATATATGCTCTGGGATGATTCATGGAAGGCAAAATGGTCC CTGAGGAGAAAATCTGGGAGAGCTGAGTGTGTGATGAAGTGTATGTTGGAGGGGAGCACAGTGT CTGTGGGAGCCOCAGGAAGCTGCTACCCCAAGATTTCGTCAGGAAAACCTA
WI-7878a	51	C G	CCAGCAACACCTACACCTTGTCACTGCCCTGGGACTCCTATGATGGCTGCTGGTTGATAATAA TCAGATCATGCCCAAGAGCGGCTCCTGATATATGCTCTGGGATGATTCATGGAAGGCAAAATGG GTCCCTGAGGAGAAAATCTGGGAGAGCTGAGTGTGATGAAGTGTATGTTGGAGGGGAGCACAGTG TCTGTGGGAGCCOCAGGAAGCTGCTACCCCAAGATTTCGTCAGGAAAACCTA
WI-7381c	213	C T	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTCTTACC AGCCCTGCAAGTTTCTCATGAGCTCGCGAGGAGCAGGCTGCAAGTTTCTGCTATGGTGAGATC AGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGACA AAAGGCTCTCTGGCTCTCAGAGCATAATCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C G	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTCTTCT ACCAAGCCCTGCAAGTTTCTCATGAGCTCGCGAGGAGCAGGCTGCAAGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C G	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTCTTCT ACCAAGCCCTGCAAGTTTCTCATGAGCTCGCGAGGAGCAGGCTGCAAGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G A	AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGCGAGGAAATTTGAACTCTCTC AGGTACTGACTGTGGACACAGAGAGATGTAGATGTGTCATTCATTCATTCATTCATTCATTCATTC CCAGGCAAGCTCTTCCCATTTTACAAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92	G A	AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGCGAGGAAATTTGAACTCTCTC AGGTACTGACTGTGGACACAGAGAGATGTAGATGTGTCATTCATTCATTCATTCATTCATTCATTC CCAGGCAAGCTCTTCCCATTTTACAAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTGTCCC

WI-1795b	130 TC	...	GAAGCAACAGAAAGTATCTTTATCCCATCTAGATTATGTCGGGTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGAGGTACTTAGATCTCAGTGCCTTGCGAAGAAAGATGTC GTCTACCATTTTACCAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAGGCAGGATT
WI-1795a	47 TC	...	GAAGCAACAGAAAGTATCTTTATCCCATCTAGATTATGTCGGGTCTCCAGACTCCTACGATTA TTAAATGTATGCATGTGAACAACACTGAGGTACTTAGATCTCAGTGCCTTGCGAAGAAAGAAAGTC GTCTACCATTTTACCAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAGGCAGGATT
WI-10616d	136 GA	...	CACACAAATTTGCAACACATTCAAAGTGAAGCCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 GA	...	CACACAAATTTGCAACACATTCAAAGTGAAGCCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 CT	...	CACACAAATTTGCAACACATTCAAAGTGAAGCCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 GC	...	CACACAAATTTGCAACACATTCAAAGTGAAGCCGCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 GA	...	CTCTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCATCTG/ANACTAATAATA AAACCCCTGTAAGTCTGCTGCAATTTTCAAGTTCATATATATCCAGTATGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTTCAGTTTCCTCAAAAGGAATATGA TGTTAAATGCAAAATCCAGCTGTAACCTTTTGGAGTGTCTTTATTTCT

WI- 10400d	189 A G			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAAATTCGCAATTCAGACATCTGCTG GTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTG(ja)TGCCATGTAG TTTTTGGTTCATTTACTGTGCAATTTATTCAAAGGCGTTAATGCAATTATG
WI- 10400c	166 A C			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAAATTCGCAATTCAGACATCTGCTG GTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTGTCATGCCATGTAG TTTTTGGTTCATTTACTGTGCAATTTATTCAAAGGCGTTAATGCAATTATG
WI- 10400b	165 A G			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAAATTCGCAATTCAGACATCTGCTG GTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTGTCATGCCATGTAG TTTTTGGTTCATTTACTGTGCAATTTATTCAAAGGCGTTAATGCAATTATG
WI- 10400a	46 T C			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAAATTCGCAATTCAGACATCT GCTGGTTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTGTCATGCCATGT AGTTTTTGGTTCATTTACTGTGCAATTTATTCAAAGGCGTTAATGCAATTATG
WI- 10809b	78 C T			AAAGGCTACAAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCACTGTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATCTGTTAG CAACAATGGAAATGTATTAGCCCAAGGCGGGTATGAGCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI- 10809a	33 C T			AAAGGCTACAAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGAG CCCCCTCTCACCACTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATCTGTTAG AAACAATGGAAATGTATTAGCCCAAGGCGGGTATGAGCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C			CGAGCTTGGGATAAGCAAGGGACCTTGGGCTCTACGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTACGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCGCCCTGGCCAGAC AAGAAGACTGTGCAAGAGGGTGGAGTCTGTAAACCAAGCATACAGTTTGGCTTTTTCACATGAT CATTTTATATGAATAAAGATCCTGCAATTTATGGTGTAGTTCGATCC
WI-7038b	140 A C			CGAGCTTGGGATAAGCAAGGGACCTTGGGCTCTACGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTACGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCGCCCTGGCCAGAC AAGA(ja)GACTGTGCAAGAGGGTGGAGTCTGTAAACCAAGCATACAGTTTGGCTTTTTCACAT GATCATTTTATATGAATAAAGATCCTGCAATTTATGGTGTAGTTCGAT

WI-7038a	31	G A	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G]A[C]TCTCAGCTTCCCTGCCACATCCAGCTGTGTG TCCCAATGAAATAC TGAGATGCTGGGCTGCTCTCCCTTCCAGGAATGCTGGGCCCCAGGCTGGCCA GACAAGAGAGACTGTAGGAAGGGTGGAGTGTGTAACCAGCATACAGTTGGCTTTTTCACATT GATCA TTTTATATGAATAAAGATCCTGCA TTTATGGTGTAGTTCGA
WI-3429b	64	G T	ATAGGCTTCTGCTGCTGCCACAGTGAACCCAGCCAGGTCGGGTCGGGCTCCACACAG[G] CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCAGAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGGAC TCCAGGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	ATAGGCTTCTGCTGCTGCCACAGTGAACCCAGCCAGGTCGGGTCGGGCTCCACACAGTGA CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCAGAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGGAC TCCAGGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTTGGCGAAAGGATAAAGAGTGACGGTGACCT GTGAGCCCCATTCTCTGATGGATAAGGTGTCCTATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786b	111	A T	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTTGGCGAAAGGATAAAGAGTGACGGTGACCT CCTGTGAGCCCCATTCTCTGATGGATAAGGTGTCCTATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786a	106	A T	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTTGGCGAAAGGATAAAGAGTGACGGTGACCT CCTGTGAGCCCCATTCTCTGATGGATAAGGTGTCCTATTGTTCTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6711b	226	G T	GGCTATTGTGAATGCTTGGTTATTGACTCCAAAATGAAATGATTTGGGGAAGAAATCCCTCACCT AC TCCAAAATCCCTACATATCAATTTACAAAAGCCCCCTAAACCTCAGTCCCAATCAGTCTGAAT TTCATATACCTCCATTTAATAATCAATACATCATTCGAGAGAAAAGACACGGTGCACACTGGGTT TGGTTGGTGCCTGCACCCACAG[G]TTGGCACTAAGTGTAACTCTCTAA
WI-6711a	36	T C	GGCTATTGTGAATGCTTGGTTATTGACTCCAAAATGAAATGATTTGGGGAAGAAATCCCTCACCT AC TCCAAAATCCCTACATATCAATTTACAAAAGCCCCCTAAACCTCAGTCCCAATCAGTCTGAAT GAATTCATATACCTCCATTTAATAATCAATACATCATTCGAGAGAAAAGACACGGTGCACACTG GGTTTGGTGGTGCCTGCACCCACAGTGGCACTAAGTGTAACTCTCTAA

WI-10613b	172 A C	...	ATTGTATGCCAAAATCATATAACCTCGCATTCAGAAACATACAGTGTAAATAAGATTTTGGCCATA TGGTGAATAATTTAGAAAGTATTATCTCTATATGATATATACACTGTTTAACTCAATGAATGTGATTT TTGTCAACTTTTTCAGCAAGCCAGGCAATTTTATTTGAC/GCCTAGGAGGTTACTATAATTTAGA AAGGCTCTACCTTCACCTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 GA	...	ATTGTATGCCAAAATCATATAACCTCGCATTCAGAAACATACAGTGTAAATAAGATTTTGGCC ATATGGTGAATAATTTAGAAAGTATTATCTCTATATGATATATACACTGTTTAACTCAATGAATGTG ATTTTGTCAACTTTTTCAGCAAGCCAGGCAATTTTATTTAGTCTCGGACTTAGGATGTAG AAGGCTCTTACCTTCACCTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG GCTCTAGTGGAAACCTCAGGTAGTCTCCGGAAGATCTGCTTTCACCAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAAJ TGGAAATGAACCACTCCCTCGCCATTCCCTATAAGAATAATCCCAAGACCCAGGCAATTTTGGCCCTCT TTCCACATGCCCCATATGTCTGAGCCAAAGTGCACCTGGGGCTGGCCCTC
WI-7587c	133 A T	...	GCTCTAGTGGAAACCTCAGGTAGTCTCCGGAAGATCTGCTTTCACCAAGTGACTACCCCTTGAAGC ACATCCCTTCTGATCTGAAGAGCCCTTGGCTCAGGGGCTGTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTCGCCATTCCCTATAAGAATAATCCCAAGACCCAGGCAATTTTGGCCCTCT TTCCACATGCCCCATATGTCTGAGCCAAAGTGCACCTGGGGCTGGCCCTC
WI-7587b	81 GA	...	GCTCTAGTGGGAAACCTCAGGTAGTCTGCTGTAAGATCTGCTTTCACCAAGTGACTACCCCTTGA AGCACATCCCTTCTGATCTGAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTCGCCATTCCCTATAAGAATAATCCCAAGACCCAGGCAATTTTGGCCCTCT TTCCACATGCCCCATATGTCTGAGCCAAAGTGCACCTGGGGCTGGCCCTC
WI-7587a	28 CT	...	GCTCTAGTGGGAAACCTCAGGTAGTCTGCTGTAAGATCTGCTTTCACCAAGTGACTACCCCTTGA ATGACTCAGGTGCACAAAAGAGCATGCTCTAGACCCCATGACTTACGCAAACTCAATCAGCCAAAC ACAGAAAAGCTAAAGACATCTTTTAAAAAGCCTTAAAGACAGCCTTTTAACTCTAAATCTG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGAGAGAGGAGGAGTGAACCTCTGTATAAAG CCATTGCTAACACTATTGCTTTGAGAGAGGAGGAGTGAACCTCTGTATAAAG
WI-10681b	103 T A	...	ATGACTCAGGTGCACAAAAGAGCATGCTCTAGACCCCATGACTTACGCAAACTCAATCAGCCAAAC ACCACAGAAAAGCTAAAGACATCTTTTAAAAAGCCTTAAAGACAGCCTTTTAACTCTAAATCTG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGAGAGAGGAGGAGTGAACCTCTGTATAAAG GCCTCTCTCAACTCTGAGCCCAAGCTAGGAAAGGCTGCTTGAGATGACTGTGTGTCCTCCCTCT AGACTCCCTAAGCCCGAGTGGACCTCAGGTGTACCTCTGTTCTCAAGTGGGGATGGG(g)TAAATAA AGAGGGGGAATTCCTTGAACAAAGAAAGCACTGGGGATAGTATATTTCACCTCGCCTTGAAGCTT TAAGACAGTATTTTGTGTAAGGTGTATTTCACCAAGACTGCAATTCATTTT
WI-7222c	126 G T	...	

WI-9826b	127 GA	AATTTATATGTGAAGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTCACGAGTTGAGCCATTGACAGAGGCTGTATGAGGCTT CAAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAGTTTCTGATCTAGATATTTAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125 AT	AATTTATATGTGAAGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTCACGAGTTGAGCCATTGACAGAGGCTGTATGAGGCTT AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAGTTTCTGATCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T	TTGTTTGTGT	TTGTTTGTGT	TTGTTTGTGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGTGGGTTTTTTT/GTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A	AGGAAACCCAG	AGGAAACCCAG	AGGAAACCCAG	TTCAAGTAACCTGCAAAATAGGAACCCAGAG/AGGGAGGCCAGGTTGGGACAAATCATGGCTACCCCG TCCCAACAGAACAGGGGAGGAGGTGGCCCTACACCCCTTAT
WI-8170b	259 GA	GCACCTTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTTGATCTATAACACACCAAGACCG TGTTTAAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAAGTTAG CAITTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAGTGAATCCCTATCAATCAGAA ATAAAGGTAAAGGCCCTCAAAATGAATCTACGGAAACATACACAAGA
WI-8170a	204 T	CCTTTATTAAA	CCTTTATTAAA	CCTTTATTAAA	GCACCTTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTTGATCTATAACACACCAAGACCG TGTTTAAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAAGTTAG CAITTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAGTGAATCCCTATCAATCAGAA AT/A/AAAGGTAAAGGCCCTCAAAATGAATCTACGGAAACATACACAAGA
WI-8172	136 C	AGGAAACCCAG	AGGAAACCCAG	AGGAAACCCAG	CAGGATTCCTTAAAGTCACTCTTCCAACTCCAGGTCCACATGGTGAAGAGTCACTGTTAAACACGAA ATCTAACCATTAACAAAGCTTTAAATCCCTCGGTAACTCCCTTTATTAATAATGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTTACATTTCTCTCACCCTTTTACA
WI-8183	56 GA	TGAAATATAA	TGAAATATAA	TGAAATATAA	AGCAGGGTTTGAATTTGATCCCTTATTTACATGAATAAACAATTTCTGTG/GAGCAGGTT TGATTTCAACACAGTTGAATCTGTAACCAACCAAGCTGTTTCTGATGAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 CT	GCCTTATTTGGGATTGCAAGCGTTTACAGGTTTAAAGACAACCCCAAGCATGGGATTTTGCAGGAAT ATTAGGGTTAAAGGAG/C/TTGAGTTGAGTCAACACACGGG
WI-8712	44 GA	AGGTAAGTGA	AGGTAAGTGA	AGGTAAGTGA	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGTAGTGGAG/G/AGAGATGTCAGGCTTCCTG TTCTTAACCAGCAGAGCCCAACCTAGAACGGCTCACTAGGCTCTTAAT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACATAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTGGTCACTTTTGGTGAAGACACATATCTGGTACAAAATT ACAGGTGGTTTAACTTACATGATACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G GTGGGCTT	GAGAACAATT GTGGGAGGAA	GGACCTATCAG TCCATGTTTGA	ATTTTGTGGCTATAGGTGAGTGGTTCTAAACTTTGAGCTTGCAGAGAACACTTTGGGGCTTAA GTTCAACATGAGCTGATAGGTCCACCCAGATTTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37 C A AAAGAGAA	AAATTTTGG AAGTTTTTCAG	TTGCAGAGGGG TTCAGG	GGAACAGACTGATCCAGTGGCAGGAAAGAGAGAA(CA)CTGAAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTGCAAAA
WI-13416	71 C A AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCATGAATA	GAAAGGCTGTAAATTTTATTTTCAAAATTTTGGAGTTTTCAGAAAAAATAAATGACAAGAAC CATA(CA)AAATATTGAAATTTATTCATTGAACTATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A AAAAGC	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTGGGTCT	TTTGAAAAAGATGCTGAATTTATCCCAAGTATAATTTAAAAAGCTG(A)TTTAGACCCCAACATA TTTAAACATCTTACACATACAGAAATTTTCAGTTTACAAATATTCAGAAAGGCATTTTCTTAAGCAG T
WI-12086	72 C T TTGGATT	CCGGGAAAC TTGGATT	GGAGTCTGG GTCTGG	GAACGAGCTTTATGGAGCAAGAGTGTGGACACTGTTTACACAAACAGTTTCCGGGAAAACTTG GATTTCCTCAAGACCCGAGACTCTCCAAAGTCTCACTGTAGTAAGGTCAATTTGGGGCAGA ACAGAACATGCTTAGCT
WI-11549	102 T G TTTTATG	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGCTTCACAGGTGTATTTGTTAAGAGTTTGTCTATCTATAATTTTCAATTTATTTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG(T)GSGGGATTTGTACAGACTTTTCCIC
WI-11585	79 T C AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAATAAACACAGGTAAATGGGAAATCAGTTTCAGAGGTAGGAAGAGCTGGGTT TGCAAAAAACAAATCTGGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGCAGGGGTAGAGT TT
WI-11604	68 C I ...			TTAGTTGGTTTCTGAACTTTATGCTGTTTATTTTAAACAAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTACCATTTTTC TTTGTACTCTGCAGTT
WI-11614c	108 C A ...			CAAAATCAAAATTTAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTGCTGTTGAGGCAT GTTCCACCTGGACTTGCCAACTTTCACGTGAAACTGCAACATATAAGTATTGTCAGCTAC GGACTTCGT
WI-11614a	60 A G CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAC ATGCC	CAAAATCAAAATTTAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTGCTGTTGAGGCAT CATGTTCCACCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATAAGTATTGTCAGCTAC GGACTTCGT
WI-11626b	83 T C ...			TTGATTTTACTAAGGTCTTCCACTGGAACTGAAGGTAGGATAGGTACAGGATAATATACTCAG ATATTTTAAATAAAT(C)TACTTAATAAAGAAATTAAGCAATACCACATTTGTCATTTGCTAC AAGAACAATTTGCAATGA

WI-11826a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCCTCCACTGGAACATGAAGTAG(G/A)GATAAGTGTTACAGGATAATATACT CAGATAATTTTAAATAAATAATTAATTAATAAGAAATAGCCATAGCCATGTTCCATTTGCTAC AAGAACAATTTGGCAATGA
WI-11827	23	T C	CCTTCTCTCC ATTGTCTC	CATTGCAAC CATCTCAAG	ACCCCTTCTCTCCATTGTCTC(T/C)CTTGATGGTTGCAATGGGAAATGGGAAAGCAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCCGATGTCAAGTCCATCCATG
WI-11838	61	A G T C T	GGACTTAAAA AGATCTGCTTA T C T	AGAACTTGGCT AAATATTTTAT GTAACACT	TCAGAAATGTTCGCAAGCAATACTATTGTAAAGGTGGACTTAAAGAGATCTGCTTATCC(TA/G)TA TATCCACATACTCTAGTGTACATAAAATATTAGCAAGTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
WI-11837	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAGAATGAT T	GTACCAATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGGAGCTGAATAAATTACAG TATACAATATTAGAGAAATATTATGTGCAATTTGCTCATCTTACTCTGACCAT(G/G)ATAATCATCTT TTTGCTGGTCCAGGACC
WI-11854	37	G C C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCCAAAAGACTATTAGCAACT(G/C)AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTTACTCAGAGTTTACACTCATATTTCATATTTT ATTTTGGGTGGTGGT
WI-11856	28	G A A	ATTGATTTTAG AAGGAACTGC	CAAGGCTTGT CCTCAAGTAAA	ACCTGATTTGATTTAGAAGGAACTGCA(G/A)CTTACTTGAGGACAAAGCCCTTGCCTGCAAGTTGTTT AAAATGTCTGAAACAATCAGATTCCAGCCTGGAT
WI-11880	55	T C	TTATCACAGC AGGGGACAG	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTTGAITCTCCCTTTT(C/J)TTGCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11896	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG(T/C)AAGGTTGGCTTCTCTA ATGCCACCACTCTTGTGTTTTCAGAACTTTTCCACTTCGCC
WI-11702	69	C T	GAATAACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACCTTCAATAATTAATAAATACTGAATAACTGAAATAACCCACAGC AG(C/J)TTTTCAGTATAATTGCTGAAGTTGTTCTAGAAACACTGCTAAATTTTGTCTGTCAGAG
WI-11706	50	C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTGTGACAATTTATTTGG(C/J)GGCTG GAATTTGCTTTTGGTGATTTGTCCTCTGGTCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTCT AATTTTACGGG A	AATATCATCTCATATCAGCATGTTTATAAAATAGAGATTATGCTCTTTTGGCATACTTCTATC TTCTTCAGACACAGAGAGAGCTTGTCTAGTTTGT(G/J)AGTCCCGTAAATTTAGAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A	GCACCTAGCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCGAGCTTCCAGCAACACCCAGCCACACTCTAGACACGCCCTTAC TCCAGTCCATCTGGCACTAGCCCTCAGTCTTTCAG(C/A)CTCTCCCTCTCCACACTCTCTC

WI-11715b	123	C T A G C T T	AGGCTGGCTGC	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11715a	49	A C A A A	AACAATCCTT AAACAACATA TCAACA	CATTACACCAC AGTTGTAATGC A	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11727	43	G C T C A A C A	AAACAACATA TCAACA	CATTACACCAC AGTTGTAATGC A	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11728	18	C G ...	ATCTGTGGTT TCGCTG	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11758	61	A G T C G C T G	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11295	37	A G A A T A A	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11773	93	T C ...	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11282	42	C G C A A G G G A A	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11790	28	A G A A C C T C T G	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11879	61	C A G T A T A C A	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-12469b	91	C T A G T T T A A A	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA
WI-11906	52	A G A T C T G A A	GCCTCACA GATTTTCTAA GATATAA	TOCCATCCTG TGGCT	AGAAATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCTTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGGAAGA

WI-11909	78 A G	TTGTGTTGGG TGTCAG	CTCTCTGAG ATTTCTGAAT AG	GCAGTTCCTGAAAGACAATGGATTGGAGCATACTGAAGACTATTCTAAATGGCTATTGTGTG GGTGGTCAAGJAGICTATTTCAGAAATCTCAGAGGAGCAAAATGATAGTGCAGTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCACTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTAGCATCAATTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCGAGTTCA/T/GIGTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATATTGG CCCTAGTGAATACAACTTTTGCTCTGGAGACJCAJCCAGCTAGTCTAAGAAACTTCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAGGGA
WI-11946	31 C A	TGAAGATCAG ATCTCTGGTTT	...	ACAAAATTCACAAGTACAACACTGCTTATTTTCTGCTTGAAGATCAGATCTCTGGTTTATTAA/T/ GATCAACATTCACACAGCTGAAGGAAATTAACCTGAACCT ACCTATTTTGAACACTGCAGAAAGGCGAGCAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTAGCTTTTAAAAAT/AAATAAAATCTGTAAACACATTTCTCATTTCTCTTACGA ATACITTTCTTTTGTATTTGCAATTTCTATGCTATGCTACACAGAGGCACTCTCAATGGCCCTG TTCTGCTGAAGATCACAACAACTTTTCAACCTCTGCTGTCAAAATAAATTTAAGGATCTTGTACCTTT GTGTTATTTTCTGTTTCAACTAAGGAC/TAGACTTCAGAAAGGCATAGCTTCCCTTGTAAAGCTTTT AAACATCTTTTCAITTTTGTAGGAAGGAACTTCAAAAGCCCAA
WI-11049	95 C T	AAAAGGACAG CCAGATATCA	TTTCCATCTTA TTTCAITTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAGTTCTCACTCTGCACATATAAAAGGACAGCAGATATCA AC/TJGTTACAGAAATGAATAAGATGAAATTTTAAACAAATTG
WI-15488	69 C T AC	AACAGTTAAT GAAACACATC	GGCTGGTGAAG TGATGTAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCGTA/JGIGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAGGTAACTTTTCCCATTTTACAGACAACCCAGT ATGAGACCTGCTTTGAACGTTAAACGTTTGGTAATAATGAAAGGAGCTAGGACAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGCAAAATCAGCCAGCTATCTGGTGCAGAGAGGTACTCCAAGTA C/TJGTTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAAGAGGAA
WI-11070b	135 C T	CAGAAATCA GCCAGCTATCT	...	ATGAGACCTGCTTTGAACGTTAAACGTTTGGTAATAATGAAAGGAGCTAGGACAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGCAAAATCAGCCAGCTATCTTJGTTGTCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAAGAGGAA
WI-11070a	110 G T	...	TTGGAGTACCT CTCTGCAAC	AACTTTTATTTCCAGCTTTGAGCAGATATTTTTGGGCTGATTTACCTCTAGCGGCGAAACCC AGAGCCAGCTAATTAAGCAGCCAGAAAGCTACAGTAATTAATGATGACCATTTTCTCTTTTAGC ACGTCTTTGTCTCTCTC
WI-12020	121 T C	

WI-11076b	142	GA	---	---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTCTCTTGGGAGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAGAGAG(G/A)AGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT
WI-11076a	106	TC	AGGCA	AAGGGGAGC	TCCTGCTCTGG GTATGTGAC GGTTATTCAAA AATTAGTATGG GACA
WI-14263	49	TC	GGCATAATCA	CGCAGAAAAA	ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAATTCGTGCCCATACTAATT TTTGAATAACCTAACTCCCTTTTGTCTACTAGAGAGTTCTTTTGGCTACAAGTAACA AATTATTCGTGAAATTAGGAAGGAGCATTCGTGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTAAAGAAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-14267	28	TC	---	CTTTTCATTT	GATTTGTTTTTATTCATCTCGCTTTTCTTTTCTTTTAAATAGAACAG(A/C)CTTTGATTTTGTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGTAGAATGAGTTCA
WI-13892	50	GA	TAGAAC	CATGAGGA	ACCTTTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGCTCTACTTTGC TACAAATTCAGATGCAGGGCATGAGAGGATTCCTCTCTGCTGCTCCAAAGGAAAGAGCTTTTGGC AATAATGGAAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCCTTCTTTGTTAATCTGGAGCA(G/C)ATTCAAGCAGCAAAATTTACTGAACACTTTGCTATGTCTG
WI-13951b	88	GC	---	GGAGTGAACA	G AATAATGGAAAGAGGAGTGAACAAAGTAATGAACAAAA(C/T)AGACCCAGATCAGAGGAAGAG ATGGCTTTCTTTGTTAATTTCTGGAGCAGATTCAAGCAGCAAAATTTACTGAACACTTTGCTATGTCTG
WI-13951a	39	CT	CAAAA	AAGTAATGAA	G GAGACCAAAAAGGCTCTGGCCATG(A/T)ATTCCTGCTCTCCCTCTGACTGACCCAGTGTTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGCATCCCTCTCTTTGGGATCTGTGAATATAACCA ACTGCTTTGTCATGGC
WI-13264	25	GA	TTGCCAT	AAAAAGGCTC	TTATTTGTTCATTAGCAAAAAGGAGTTAAATACTGATAGAG(A/C)ATGCAAAATTTGCTCTTTATGCA TTTGTGGACAAAGTACTAATCTTGTTCAC(TG)TCACTTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39	AC	TGATAGA	AGTTAAATAC	AACTCTTTATTTTATAGTAGCCCGAGTACTTTATGCACTCTTAACCAAGAGCCCTTCAG(C/T)AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTGTCTCAGGGTCCACCAGGAACAGGCTTTGGCT
WI-15843	62	CT	CAG	AAGAAGCCTT	

[illegible]

WI-14297	86 A T G	AATGTTGGGT ACITTTTCCAA	TGTGCACATC AGAAACATTTT	CTGACITTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTCAGATTATAAAAAAT GTTGGGTACTTTTTCAGATTAATAATGTTTCTGAATGTGCACACTAGAAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G A A A	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTTGJACCAAAAAATTAAGATTTTTCGGGCAATTCACATGTTT AAAAAT
WI-13582	43 C A A G A C T G G G A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGACCAATGCAATCTAGAGACTGGGACATGGAATCTAACTGGCGCAGAG AAATCAAGACCGATGTTGTAATCTGGGCGAGCTTCAAAATTTCTGCCCTCAAAACATTTTCAC CCAAITTTTTCATTATGGC
WI-13857	28 A G		...	TCTGAGTTGATAAATGCTTTTCTGAACTGATACAGTACAGATTTTCTGATGTCGCTCCACATCTG CTGCCAATTTTGTGTAGCTTTTCAACAGTACAGATTTTCTGATGTCGCTCCACATCTG
WI-15809	77 T G T G T A A A T G C C	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATCAATGTTT GTAAA	GTTTAAAGTTCAGAGATGTGAATGGTTTACAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCCCTGTTTACAACATTTGAATAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T		...	TTAATCAGTCTGTGCAAGAGAAACAGGACTTTGATCAAGCTCCAGGCTCCAGGCTTATATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGAAATGGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G A A	CATACTCCACT CTAGCTGCAAT	AGAAGAGTGG ATGGGATGC	TCITTTTATCCAAAGATGGGAGCGCAATTTTCAATGGCTTGAATGAGAAAGCTTCTACTCCACTCTA GCTGCAGTAATACTGAGCATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A A A T G G G A A G C	TTTATCCAAAG AATGGAATG	TCATTCAGCC AATGAAAATG	TCITTTTATCCAAAGATGGGAGCGCAATTTTCAATGGCTTGAATGAGAAAGCTTCTACTCCACTCTA GCTGCAGTAATACTGAGCATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-13783	59 T C G C A G T G A T	GGCTGGCACT CCACACCTGC	CCACACCTGC CCCT	GCTCGTAATGAGACAGACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGTATTCJAGGG GCAGGTGTGGGGAGGGTGGGGCTCTGAGCCGAGACAAATGTCATGGCAGAGCTTCCAGAA
WI-13578	48 T A A C C	TCATAAAGA GCAGAAAGAA	CAGTGTGTAG AACATCTTTT GTC	TTTTTTTGTGTAGTGTGTTCTTCAATAAAGAGAGAAACCTTATGACAAAAAGATGTT CTTACACACTGAGCTTTACAGCTACCCCAACATGATATTTGCTTTTCCGAGGCAAAAAAGA GAGTCTTCCAGAAACCTC
WI-13789	62 G A A G G G A G	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAGAAAGAAACCAATGATGAGAAACTCAAGAAATGGATGGCTGAGGGAGG/GA GAACAGAGGAAAGGCACTGGGGCTGGGCTGAGTATGACAGTGGATGGTGGTCTCTCTCTT GAGGTCCCT
WI-13594	66 G A A G C	TTTTTAACACA GATACAAAA	CCTTTGGCCA GTACTTTT	AATAACAAGTTTAAAGTTCAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCACAAGAGC GATGCACAAAAAGTACTGGGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40	CT	GTTCCTCCACCTACTCCGGCAGAAAAAGGCATATTCAAC/TTGTCCCATACTAAATTTTGAATAA CCTAACTCTCCCTTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
			CCACACTGAA GACTCACCGAG		TCCCCACCCCA CCCT	GTCTCACTTCTGTGTAGGCTGTAATTTTACAGTTTAAAGTTTCTATGTGATTTGTGGCCACACT GAAGACTCACAGAA/C/GJAGGGTGGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCTCT
WI-13367	84	CGA			CATATTGAAAA TTGTTACTAGA	CTCACITTTAATGAGCCCAAGCATCCAT/GJCCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAAGAATACCGATTGTGTAGGGAAGAGCATAGAGGACCAACCATCAGCAACCCCTCT TGATTCCTCTCTACCC
WI-13600	28	GT	TTAATGAGCC AAGCATCCAT		GCATACCTCAT GACAATATTTA	GATAGGAAAGAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCC CTTCCATTCTGGAGACAACACA/GJAAATCTATTAAATATTGAATATTGTCATGAGGTATGCACCT GCCCC
WI-13602	89	GT	TCCATTCTGGA GACAACACA		ATATTAAAT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAGATTTCACAATATTTCAC TTTAAACAC/ATTTAAAAAACTACTCTTCATATCTCTAGCCTGATGACTTAAAGTTACCGG
WI-13650	76	AT	AAAGATTAC AATATTTCAT TTTAAAAAC		CAGCTAGGAT ATGAAGAGTA GTTTT	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG/C/JACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAAT
WI-14319	83	CTA	CAATACATT GCATTTTCCTA AGAAAA		CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAACTCAATACATTTGCATTTTCTTAAAA AAGAAGACATTT/GJTTTCAGAGAAACTGTGGTATCATGCAGGAAAGCAGAAAAAAATTT ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTTCCAGTGAAGTTCACTCTCTCACACT CTCTTCAAACTCGAATACTTTTCTG/JAGATGCTAGCTAGTACCACCTGCCAACTCTCTCAA
WI-13909c	93	AT			...	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTTCCAGTGAAGTTCACTCTCTCACACT CTCTTCAAACTC/GA/JAATATCTTTTCAGAGATGCTAGCTAGTACCACCTGCAACATCTCTCAA
WI-13909b	80	GAC	TTCTCACACT CTCTTCAAAC		GCAGTGGGTAC TAGCTAGACAT CTC	TTTTTATTGAATCCAAATGTAGCAAAATCAATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC/C/JATGGGAACCTTGAAAGGCGATGGCAGTGGAGACCAAGTAACCTA
WI-14323b	86	CA			...	TTTTTATTGAATCCAAATGTAGCAAAATCAATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC/C/JATGGGAACCTTGAAAGGCGATGGCAGTGGAGACCAAGTAACCTA
WI-14323a	78	TCACATCA	ACAGAAAAAT TAAGAATCAA ACATCA		GCCTTTTCAAG GTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCAATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC/C/JATGGGAACCTTGAAAGGCGATGGCAGTGGAGACCAAGTAACCTA
WI-15389b	104	GAAA	AGATAATGAA ACATCTGCGA		GATGAGGTGAT TCCCCACATT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAGACTACCATTTTCAAAATTTATGT AATACACTCATCCAGATAATGAACATCTGCGAAAA/G/JAAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 GA TC	AATCAACTAG CTGCTTTTGG	TTGTAATAATG GTAGCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCCTTTTGTGCTGTAATTTGGAAGACTACCAATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAGTGGGAATCACTCATCTGTGCTG
WI-15747	88 TC AGTGTT	TGCTTCATTT AAACTAAATTT	CATAATTCACC AAAGTTTCATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAGACAGACATATGTTTTCGATAAAGATATAAAATTTGCTTCAT TTTAAACTAATTTAGTGTTCCTTTTAAATTTATGAACCTTTTGGTGAATTTATGAACCTGTACCAAAAC C
WI-13752b	117 CT	AAGAAAGCACATACATATTCAGAAATTTTGGAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTTGGCTTGCACCTTTTACG GAGGATTCGCGACAAC
WI-13752a	106 TC AGTCTGGA	CCTTCTCGTTA AGTCTGGA	COCTCOGTAA AGTGTTCC	AAGAAAGCACATACATATTCAGAAATTTTGGAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTTGGCTTGCACCTTTTACG GAGGATTCGCGACAAC
WI-14339	102 TC TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTATGAATGTTTCCAAACACACCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCAACCAATCAACAGTACATGATTACTTCTGGTTTCCAGAAATCTGGATAC
WI-13744	115 CT AAACTGAA	TGGTGCTGAAC GATAAGCACCA	AATCAGGAAA GATAAGCACCA GC	TGGATGGATGGATGAGGCCCTGTGTTCAACAAACACGTAATGGAACCTTTCATGCGAGCTTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGCTGACAAACCTGAACCTTGTGCTGTCTTATCTTTC CTGATTTCT
WI-14081	68 CT	CCTTTGACTATATTTGTTTTTCCAAATAGGACTATGTGTAGAGAGAGAGCCCGGTACATACCTTAT CTTAAACCATTTTATCCACCATTTTGTAAAAATCTCATCTTCTGGGTCTGGATACCTCAAAAACAGAT
WI-15719	69 AC CATTGAGC	ACCTTTTCATC CATTGAGC	TGACTTTGGC AAGAGTTTAA ATT	TTACAGTTGGATTAAACACTACACACTGAATATACTGAATTAACCTTCAACCTTTTCATCCATTCAG CTATTAATTTAAACTCTTGGCAAGTATCATGAACCTTACGAAGAGGAGATAGAGATCTGATC
WI-13810	106 TC AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCAACATCACTAGATCAACAGAAAGTACCACAGTATGCTTTATTTTGGCA GGTATTAAATTTGTTCTCTAAATCGATACATCCAAACTTTTCTAGTACGAGCAAGCATCAGTTCTTTC
WI-15736a	27 GT CACA	ATTTATTCAC ATTAACTTG	GTCTTTTGATA TGTGCTTAGT TTT	GGATTTTATTCACATTAACCTTGCACAGTGTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 GA	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGCCTGATAGTACACATAGCTGTCAACACACAGTG
WI-13785c	56 AC	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGA AACAAAGTGGTAGTACACATAGCTGTCAACACACAGTG

WI-13785b	40 C G ...	AAAAGTGCAC ACTATAAAG	... TGTTGTGACAG CTATGTGTGAC	TCAAACTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACACACAGTG
WI-13785a	27 T C T G C T T	GGATTTTACAT TCAGCCTAGAT	T TTTGTACT	TCAAACTGCACACTATAAAAGTGCCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACACACACAGTG
WI-13793	88 C G A T A G G	TTCTCACCCCT TTCTTCTCTC	AGAATGGGCTC TTAACCCTTGA	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTACCCCATTTGATACACATAAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCAATAAATCTATGACTTG
WI-13794	52 A G T T T C T T C T C	TTCTCACCCCT TTCTTCTCTC	AGAATGGGCTC TTAACCCTTGA	TAGTCTCTACAAATTCCTTCAATCCATTTCTTCTCACCCCTTTCTTCTC[J/G]TACAAGGTTAAGA GCCCATCTCTCAACAAACAAACAAACATAGAGCAAT
WI-15729	35 A G G T G A G A C T G C	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[J/G]GGCCTTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTGACTTCCAGGAGGGTAAGTCCCTGTTTGACGCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACCCTATCTT	TTTTTCTCCOC AGGGTCTA	GTCCCTTGACACAAGTCTCCCAACTGGTTTGGAGTTTTTCCCTTCTGAGGTTTTTACCCCTATTCTC[J/G] ITAGACCTGGGGAGAAAACACATGTGTAAAGTGGCTCAGGACATGAGCGAGGCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C A A T T	TCATTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/J]GAGATCCAGATTCAGCTTGTCTCATATAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCTGAACATTTCTTGAAGCAGAA
WI-13446	22 C C T C A C T C A T C A	GCCATGTTCTT TGAGCACATA	AAGGGAATCA AATCAGAAG	TGCCATGTCTTTTCACTCATCAG[C/G]CCTCTGATTTTGAATCCCTTTCTGCTCTGTAATTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTGAATTTCTGTTTTTGGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCTTAAT
WI-13725	56 A C T G G G T G C C	TTGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGAAATGTCACTTACACATGGTGAGCACATATGGGTGC[C/J]GCCCGAG ACAGCAGGATAAGTTTCACAAACTTGACAGGCAAGTTAGAGCAAGGCATGGTTTCAAGATG
WI-15702d	107 T C ...		---	CAAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTTCAAAAGGGGGTAAAGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAACT[C/J]ACTAATGGGTCTTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ...		---	CAAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTTCAAAAGGGGGTAAAGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTCTTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ...		---	CAAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTTCAAAAGGGGGTAAAGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTCTTTTGAACAAATAGTTT TGA

WI-15702a	48 GC	AACAAATAA AGGCTTCAA AAAG	CCTCACCCCTT TACCC	CAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTCAAAG(G/C)GGGGTAAAGGGTG AGGAAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAAAGGGTTCTTTGAACAAATAGTTT TGA
WI-13831b	113 TC		---	TTTTTTTTATGGATGGACTGTACATGTTTATTAGCGAAGGTGACTTGGAAAAGGAGATTTCACAT ACTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGAT/C/GTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13831a	56 GC		---	TTTTTTTTATGGATGGACTGTACATGTTTATTAGCGAAGGTGACTTGGAAAAG(G/C)GAGATTCA CATACTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGATGTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13808	82 GA		---	TGATTGAGCTTAGAAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAAGTCCAGGT(G/A/C) CCATTAGCATGCTGTGAATGCAAGGAAAAGCTTAAAAAATTTTTTAAAGGGTGACTCCAGTAAA CAT
WI-14372	86 AG		---	CACATTTTCAGCAACAAATCGAGGTGCAACACAGGGTTTATTTCACATTAATATTAACTGGATT TTTGCAATAATAGGA(G/G)TCTCTTTAAATAACCATCTCCTCATTCTATGGCCAGT AGGCTGTTTTTTGAGGCTGAGGACCCCAACATGACAACTGTAAGACTGTAAACATGTCATGTGAGTT ATGAGCTAGGAACCCCTGGACGAAACCAAGCAATACATATACATCATCTCCCACTCCCAACGCCCTTT ACTTTCAGCCCTCTGCA
WI-14373	95 AG	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTTGTCATGT CTCTTACTGC	AGAAACCAGAACTCAAGAACCCACATGGTGTATCAAGAAGTAAATAGGAAGAGCAAGA(C/T)G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47 CT	AGACTTGAGA GCTTAAACA ACACT	GCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACACACAC(T/C)TATTTGTTATTTACAG CTCAGTAGTTTAGAGGTCCAGTAGGCTTGCTGAGTTGTTTCTTAAGGTCTTACAAGGCCAA
WI-14085	31 AG	CATTTATTTT ATGTGTAAGA AGAAAAA	CAGTCATGTC ACGTGCTAGTT	TGCAATTTTTCATGTGTAGAAGAAAAAC(A/G)TAACCTAGCACGTGAACATGACTGCATGGATAC ACGGCTCAGCAGGAGGCTTAAAGTCAGAAGTGAGTGAAACAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCTTT
WI-12169	121 GC	AATAAACTT CCTATTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTGGCAATTTTATTTCACCTATCAAGAAGTACAAAATATTTTGTTCATTCTTAA TTTTACCTTTTATGCTAAGTTATAAAATAAACTTCTCTATTCTTTTCTT(G/C)TTTTTCTTCA CCTCAGAACCCCTTA
WI-15705	50 AG	GGAGGGAGAT TTTAGACTGA GATC	AGCTGTAGTGG TCAAATACTCT AGAA	TTGTTTTTATTTGGGGAGAAATGAAGGAGGGAGATTTTAGACTGAATC(A/G)TTCTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGACTACGGAGACCTGCTTATAGCCCCAACAGGAATCTCTCA TCTGGGGTTGGCAGACAG

WI-14379	102	C T	CAAC	TCTATTAAACA GGGTATGTCA	ATCATCTGTT TGAGGTTGACA	TTATGCTGTTGTTTCTACTGGTGGTGGCTGCTCACTAATATCCAAATCCTAGTATGATTTCTTT TACTTGTCTATTACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCCACTTAAACAAGAGGACACTGCAGAGGCTTATGTACA ACAGTGTCCCGCAGGCTGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGAGCAGAG
WI-14102	22	C A	...	CCGAGAGCTG CTGTATTAA	GCAGAGATCCA GACGCTGT	ACCGCAGAGCTGCTGTATTAA[A/G]ACAAAGCTCTGGATCTCTGCAAGGGCTGGGACCACTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCAACCCC
WI-15937	24	A G A	...	AAACTGAAAC GTATTCTCTC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGATTCTCTCCA[A/C]ACACCGTAGAACTTAAAGCCGCAAAAGACTCACACCC ACCACTAGCGCGGAAAAAGGAAGTTTCAGGTGATACAAGATGCTCTGCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAGGTGAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGGTTAACACTAAGCC[A/G]ATTATTCAAAATGTGTTTCAAAATACTACAGCCAGAT CACCAAGCTCAGTCACTAC
WI-14124	92	A G	...	GGTTGACCTG CATAGATTTT	GGATGGCATG GOCAC	GACAAAGAGCAGTTTCTGTAGTTCCAGGAGGCCAGAGCAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCAGSACTA[C/T]GTGGCCATGCCATTCTGTAAAGTGAAATTAATGAACA
WI-14125	88	C T	...	GCCTTCACCC ATGCTTCACA	CTGTTCTGTC TCTTTGGGC	GTATTTTCTCACAGTTCTGGAGTTAGAGTCTGAGATGAGGATATCACAGCATGGTTAGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTTTACAT[G/A]GCCCAAGAGAC AGAACAGCTCTCTGGT
WI-14136	120	G A	...	TGTTGGACCA GAAAGCT	CAGTATGTACA GTGACATAACA	TTGTTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATACTGTAACAAGACT GCATTAATATGTTTCTTATGATTGTTTCAATG
WI-14138	23	C T	...	TCCTCAGTAG TAGTATTTCA	GCTCATTTCTT TTAGTCTAAG	GGCAGGTTATTCTATAATTTCAAACTTGGAAAGCAACCAAGATGCTCTCAGTAGTAGTATTCA GACAACTG[A/A]ATATTACTTAGCAGCTAAAGAAATAGCTATCAAGTCATGAAAGACATGCAGG AACCITTAATGGATATTACT
WI-13551	74	G A	...	GACAATC	TAATATT	TTTTTAAAGAGTCTCTCACATCTTATATGTTATGTCACACAAACTTTTTAACTCTCTGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTCTTTTGGATAGAAGCCTCTTTCAGAAATCA CCTCC
WI-15953b	59	C T	...	TTTAAAGAGTG TCCCTCACATC	TCATCTGTTCT TGTTGTTTTG	TTTTTAAAGAGTCTCTCACATCTT[G/T]ATATGTTATGTCACACAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTCTTTTGGATAGAAGCCTCTTTCAGAAATCA CCTCC
WI-15953a	26	T G A T	A	TTTTTAAAGAGTCTCTCACATCTT[G/T]ATATGTTATGTCACACAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTCTTTTGGATAGAAGCCTCTTTCAGAAATCA CCTCC

WI-14631	82	G A	TGAATTCATGGACAGTGTTCGCTCTGTTTAGTGAAACCCCTCAACGCACTCTGCAATAGTCGCGCTTTCTGTCTCTTAAC[G/A]TGCCTGGTCCCTCTGCCAAACCTTTAGGATGGGCTCCTCAGGGCCCTTGCTCTG
WI-6053	24	A G	ATCACACCGTGTCTAAGAACAAC[A/G]TCTTCATGTCCAACTCATATCCCCGGGACTTTTGTCAACTGCAGTACACTTCCTGCATGAACCTGCCTCTGGAGGGAAGCTCCTAGAGGCCAGGTAAGGGGGTGCGAGCAGTGGGGGTATATCTGGGCTGGCCAGTTTGAACCCAGGAG
WI-15964	99	T A	CTGAGGTA	...	CAGAAACCTTCTGTGTATTAAGCTGTAGGAGGATTAATGACAGAGGCTCCAAAGGCAGGAGGCTGCCTTCAGGAGCTGTAGAGCTCTGTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAAGTCTTTGGCAAGGGAGCTTAAGGTAACCTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAATACCCATCAGAGACAGTGCACAGGAGCAGCTGGGGCACGGGGGACGG[G/A]GAAGGAAGAGAAGAAGGGGGAGGAGAGACAGTGCACAGGAGCTGGGGCACGGGGGAGGG[G/A]GAAGGAAGAGAAGAAGGGGGAGGAGGAGTGCCT
WI-12075	103	G A	GGCAC	...	TAAATTAACACACGGCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTAGAAAGGACATGATAATAGTGTGGAGTACGGTGGAGGTCA[G/A]SCATCTACAGGGTCATTCGAGGAGGSAACAG
WI-12179	96	G A	TGGAGTCA	...	CACAAATAGTGAATTTATCTGAGCAAGAATCATCTCTCAITTTAAATTTGTIC[G/A]AATAAGTCAAGAAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTCACAGGTAAACCACTGTTTAAAGTGACITTCACCAAGGGTTTAAACCTAATCTAATACAAGTCTTACAACACTTCCAGAGCATATATAACAAGAATTTATTCAGGCGAGCTAATGTATTAAT[A/G]AACCATGAAGAAGAAAAAATCTGTATCTAGATGCAGAAATGGGCTGGAGCTGTCTGTCTGTGTAGATGCAGTGTGTGTATTTCTACCTATTACAAAATTAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATACAGTC
WI-14666	105	T A	AATTTAATAGCAGCTGTGTGTGTGATTTTAAAGAACAGATAAAATATGTCAATTCAGCAGCTCATTTAAAAATAAAGACTACAGATACAAGGAATAAAAA[A/C]CACTTTTAGGAGATGA AAAACACAAA
WI-13473	31	CT	TTAATATTCAGCAAAAGTTATTGCAACAGGTTGAAATGCGACACACATATTACAGGCTGT[A/AA]AACAAATGAGTTTACACAATTAATAATTAAACACATACTTATGGGATTTGTGATGA
WI-13967	103	A C	AAATAAAA	...	TTTGTTGTGTA
WI-14408	60	T A G	TTTACTTT
WI-13683	47	C G	TTGTAATATTATATAGTCGTTTATGTGACATAITGATGTC
WI-13910b	63	CT	CGTCT	...	TTAGAAAACCTGATAAAGCAACAACTTTTGGGAAAGCAACCATGGCAGCTCCTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14525	22	G A	ACATGGCAGATACAGAGCTGT[G/A]TCTTTGAAGACACCACCTGACGAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATGGAACAGTTTTCCTGACCCTCTGGAGCGTTGAAGGGGTGACCAAGCACATTTCGCATGCAAAA

p.

WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCATCTCTCT TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCAATGATAACATAAAATGATCATGAGAAATTTCA/T/CJGTTA AAAGTCAAGAGAGATGGCTAATGATGCTGGGCT
WI-15361b	101 A G A	CCACITTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTATTAAGCCATCAAAATTTCTTCACTCAATACACTGTGTAACAACAAGATAACACAT CTTCTGTCTCCTCCACTTGAAGTCAAGTCAATCAAGTTTAGGCACAAAGGTTTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T C	GCGTTTGACTT GTGCGG	TCCACACTGC OCCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAATTTGGTTTATTCAAACTTCTAGCGTTTGACTT GTGCGGTC/TGCTACTCAATGGGGGCGAGTGTGGAGCGGAGGATTGCAACCAGAGTTTCTACTG CAA
WI-12535	50 A T T A T	CTAGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCTTAACATTTATTTCAGGTGGTACTAGAGAGGTTGAGGTGTAGATATTA/TCTTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTCTTGTGTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A G G G A A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATGCTTGGCTTTACCAATTTTATAGCTATTGGAGGCGAGAAAGGGAAATTTTGGC COCAGAAACCATGAGATTGGTGAGAAAAGGCACACGGGAA/GA/AGGGTCAAGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	ACACAATATAATCCATTTC/CJGAGTGTATTAAACCTATTGTGTTTAGAACCAACAAACTAG AAGAAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A C T A C C C T G T	ACCCACCACA CTACCTGT	GAGCATCACA ATGTTAAGATT TT	CTTTGAACACCTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCCTGTTT/AJAAAACTTTAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAACAAAGAAACACACAACTGAAGGCCCCCATGTA
WI-14816	29 A T	AGTTAAAAAAATCGAGTCAAGATTATTATTAATAACTGGACACGCTTCTATATTGCAAGCTCAT TCAATGCAATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAATATTACTAAAGGAATGTTG ATTACCAAGTACGACTTC
WI-12542c	71 G T	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T T T T A A A	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAACTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGCTGCTTATA GAGCATACATTTCTAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ...	TGGTGACAG GAAATACCT	TTGTTGCTA CTTTTACAAA CTTT	... TTGTTGCTA CTTTTACAAA CTTT	TTTGGAGGATAGAGACAGAGTGTTC/GTGTGATTTCCTGTTGCGTTTCAGTTTGGTGTGTCATT GGTTTGTGTTTTCCTAATTTTGGCCACCTATAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60 A T AA				ACATTCCTTATGATAGCAACAACCTAAATATGATGGATGGTGACACCGGAAAAATACTTAAATATTA AGTTGTAAAGTAGCAACAATAATGGATATAGTATATCTATAAGTGATAGGATGTATATGAAAAA GGCTATAAAAGCTCCAAA
WI-14863	61 G A	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAGGGCAAAATATTTTGTCTG/GA/JAG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATATTTGATTGCCACT ACGTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTTAAC	TGGGCTGCAG ACACTC	...	TTTTAATTAAACGTAAAGGAGGACATTCOAAGGCTCTCTAAAT/C/GAGTGTCTGCAGCCCCA TTGCTTTGAGATGTGAATGTGTAAACCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATCTGC	GATGAGGTGAG GCCATTTATT		ACGAGTGTCTCTGATGTATCTTGTCAAAAATGTTTGCCTGATCTAATCATGAAAGAACAAAT AGAAAAATCCAAATTCACAGATATCTGCA/GA/AAATAAATGGCTGACCTCATCAAAAACATCA ATGTCATGAACAAACAAAA
WI-14898b	79 A C	TTTTGTACCTATCCCTGTTTCAGTGCATGTACAGGAAGAGTGTCTCATAAGGTGCCACTAAGGAAA ACTTCTCCAT/C/JAAGCTGCCTGTGTGCACGTTGCCTGGGCTTTTGTAAACCCCTGGTGTGCTGCT GCCTGTGTGTCTCT
WI-14898a	50 A C CA	CATGTACAGG AAGAGTTGTCT	AAGTTTCCCT AGTGCACCT		TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTGTCTCATA/JC/JAGGTGCCACTAAGG AAACTTTCTCCATAAAGCTGCTGTGTGCACGTTGCTGGGCTTTGCTAAACCCCTGGTGTGCTGCTG TGCTGTGTGTCTCT
WI-14907	48 G A GGACTCTGAC	GGCACACATT GGGAAT	TCTGCTGCAAG GGGAAT		TGGTATTTATTCGACACATTCTGTAGAGGCACACATTGGACTCTGAC/GA/JATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCCATCAATCAGTGACTCCTGCACAGGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGGT	CAACCAGGA AAAGGAACCT		CTAGAACTCTGGGAAGTCCAAGCTCAGTGCAACCAATACATTCAGTTCCTGGTGTG/JA/JAGGTCTCTTTC CTGTTTGCAGACAGATACCTTGTGTATCTCACAATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A	CTGATGCTTTGACATCTGGGGCATTTGCTGTCTAGAGAGACTACTTCTCTGGGACCGCCAAATTC TAGTGATAGTAGAGGACTCA/C/JCCTGCACGTCACCTTTTCATATACAGATCAACCAATCCAAAA CTACACCTCCAAACCCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCAGGA CAATAAATTC		ATTTCTCTGATTTGGCTGTCTGTAAGCCCTGTGAAGTCAATGCACATCTGGACACAGTTTCTCTAGCA/G C/GAATTTATTTGCTCTGGGCTGTGATGGCTTTTCACAGC
WI-14926	49 T C ...				GTTAATTTCAAAATGACACATCCAGATTGAATGGGCACCTTAGCGAAT/C/JACTTGTGGACCACA AGACTTGTCTGAGAACATGTTTCAAGACAGTTTTCAAATAAAAAATTTTCCCTTAATCAGGTCCA

WI-16083	89	C T	ATGTTAACA CAACATATC AAGGAT	TGGAAAGATT CCAGCC	GCATCTTTATACACAGAACTCATTTATGTCCTTAATCATGTTTAAATATAATAAGCATGTT TAACACAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55	C T	GGAGGATC CTCATGGAT	CACAACCAAC AATACCG	CAGTTCTGTGTTCTGAAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTGGTTGGTGATTGGGGAGCAAGGAGAGCAA
WI-14946	47	T C	TCAATCTGAAGGTCTCAAAGTGGTCTATTGCCCCACAGACATAACAT[C/T]CTCTAAATCATCTCTA GATCAGGGAGTCATAAGGAGCATTAAAGGTCCTCAACGAGTTGGTAGTGCCTCCACTATGTGAGGACAC
WI-15987b	80	A G	ACATTAAACACAGACAAATTAAGGGTCCCAACGAGTTGGTAGTGCCTTAACCTCTCAGC TAAGAAGATGGTCAG[C/T]CTATGAACCAAGTCGCGGTCCCATGCTTTAAACCTCTCAGC
WI-15987a	32	C T	CACAATTAAA GGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACAGACAAATTAAGGGTCCCAAC[C/T]GAGGTTGGTAGTGCCTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAAGCTGCCGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	55	T C G	AGGGAACCTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTATTGCCGTTCTTCCAGGAACAGGGAACCTGCTAAGTGTCTCAGT[C/T]CCAAACA ACTGATGTAAGATCATCTCTGACCATAGCAACCTGTAGGCTTGTCTCCCTCCAGCTGA
WI-16100	52	A G	CAAAAAGCTA TTTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[C/G]GTAAATATACTG TTTTCTGACATTCCTGTTATCAACTCTCTCTGAAAATC
WI-14958	83	A G	AATAATTTAT CTCTTCTTTT CAAGCG	AATGCATTCAT TTGGGTTT	GTGATTGATCTGTAATTATGGGATTATTTTCAACTCTAAATTTCCAAAGTAAATTTTATCT CTTCTTTTCAAGG[C/G]AAAAAACCCAAATGAATGCAATTTTTCAGTTTCTCCAGGCTTTGAACCTGC AGCAGAAAAATTCAGGA
WI-14976	35	C T	GTGATTTGCT TCAGTGGTGT TATTGGATTT	TCAAACTAAAT CTTCCATCTA AGC	TATTTTAAATTTGGTTGTTGCTTCTGTTCAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGCATAGTGGCCACAAAGATGCCCCATCTCACACCTGGAG ACGTCCATGACACCTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATACCTAGC ATAAA	TAATGTATTCAGTGGTGTATTGGATT[T/G]TTTATGCTAAGTATTATGTCAGAGGTGGAGAT AAAGAGGAAAAAGAAACAAGTGTGCTCTCGCATCAACGACCTGATCTTGTCAAGGAAGTTTTTGA GAGCTCACAAA
WI-14982	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTCCCT	TGATTACATTTTAAATCATGCCTACAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA ATGAAAGTTGCA[C/T]AGGAAAGCTGAGCACATAGACCCCACTGATCGGAAAGAAACGTA
WI-15002	72	T A	AAATCTCTCTTTCACACACAGATGAACCTTTAAATAATACAAATGCACTGAAATGCCTCTTGA TTTCTCTTATTCAGTTTAGGCTCAAAATGGGCTCTCTCAAGGCTGGACCTCAAGGCTCCAGTT
WI-15000	90	G A	GACAGAAAA GACTCAGACT GTCTAA	GTCTCTAGTTC TGCAAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGATAGACAG AAAAAGACTCAGACTGTCTAAGTATGATGAGTTGTGCAAGACTAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTCATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCAGTGCACAGAGGACTCACACCTGTGCATAGACAGCACCC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA TAAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTCAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACAAT/TCAAAAAACAACACTGGACATGCCCTGAAATGCAAGT TGGAGTTCTGAAGAATCTAC
WI-13470	100	C A	CTGCTTTAT ATTGGAATTC T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATAGCACCTGAAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCAAGTGAGGAAGCC AGGGCACCTCAGCCCTC
WI-14712	38	T A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCAT/ATCTCACAAATACCATATACAAACATCT TTCAATCACAACTCAATATAAATAACCTACAAATCACATTGC
WI-13712	40	C T	TTTACTTTTGT GTCAATTTTAT CTCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTGTTGTGCTATTTTCTATTG/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATGGCAATATGCAATATAATTTGTGTGTTGTTAAATTTATGCAT
WI-16163	35	C T	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACCTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA/C/ATTTGTAAGTTAATGTAATGGCAGCAT GCCAAAAGTTTAAAGAGACTATTCTTTTAAACAAGACAGTGTCTGACATTTATTTCCAGGT
WI-13453	88	T A	AATGCACAAA ATCTGTCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTTGCATTGAGTGTCTTATATATTGGGAATTGCAGTGATTTAAACATTGTACAAAT GCACAAAATCTTGCTCTCTG/ATGCTAGAAAAGAGATGTAAAAATCTGCACCTAGTTGAACAGTCTT AATGAACTCATTTGCCAT
WI-16167	58	T C	CGCACTCTAA ATTAGAGATA GATTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATTT/CJCATCTT ATTACCCACGAGCACACACACGACAGTAGAACAGTTCACACCTGATAAATTGCACAAGATG
WI-14482	17	G A	GCAGAACCAATTAATAAG/AJAACTGCAAGTTTCCCAAGAACTCTGGAACCCATAGTGCCCTAAT GCCCTTTAAATCGACTACTAAAGGAGAGAGATAAAGAGAGTGTGTGATGTGACAGTCACTGGT TGAGTTCTTCAAAGACATGTTGGCAGATAGCCAGGCCACTATGTATTTCCAGTATCATGTAC
WI-15069	81	T C	GCACATAAAAAAT/CJGTGTGCTTGTGCTGTGTGAGTGAACCATTTGCTTTAAGATAAA ATCTGGTATTGTGTATCCCAACAGTATACAGAACTACTCTATAAAACCAACCCACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/CJCTCTCTCTCAAAATGCACACAAATTAAGACG
WI-16156	97	A C	TGAAGATTAA CCAGAGTCCG GCAGCAAGAT TACATCAGTA	AATTGTGTGCA TTTTGAAGAGA CTCCAATAGC CTAGAGTATAG TAAGGT	ATCTGGTATTGTGTATCCCAACAGTATACAGAACTACTCTATAAAACCAACCCACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/CJCTCTCTCTCAAAATGCACACAAATTAAGACG
WI-15012	59	G T	ATGT	TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTCATTTGAAGCTTTG/TTTACCT TACTACTCTAGGCTATTTGGAGTGTCCCCAC

WI-15100	74	G A	GTCAACATGTT ATATTTCTTT TAAGAC	TCATTACAGCAAGCAAAAATACCAATATTTCCAAATAAAGCAAAAATTTGGAACAGACTGGA GTGAGAAQ/G/AGGTTCCACCACCAAGCCCTCAAGACAGATGACCGGCACTGGTTCTGGGGT GCATTTCTAGTGGACTTAT
WI-14492	92	A T	AATTA	...	CCCTTAATTTT CCAAATATAA TAAGAC	TGGTACAGATGTTTAAATACAGCAGGCGAGTTCAGTTAAATATAAATTTAAACCTTTATTTT CCCAATATAAAAATTAATAATTAATTAATTTAAAGAAAATATAACATGTTGACAGCTTT TCTTTAAATTTTATCGGAATCCAGGACACAAAGAAAACACCCAAAACCATGGAGACAGAAAG ACGAGACACAACTCTCCCCCACTGCGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C	TCCTTAATTTTATCGGAATCCAGGACACAAAGAAAACACCCAAAACCATGGAGACAGAAAG AC/G/AGACACAACTCTCCCCCACTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A	TCCTTAATTTTATCGGAATCCAGGACACAA/G/AGAAAACACCCAAAACCATGGAGACAG AAGACGAGACAACTCTCCCCCACTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G	GGACAA	...	TCGGAATCCA GGACACAA	TCCTTAATTTTATCGGAATCCAGGACACAA/G/AGAAAACACCCAAAACCATGGAGACAG AAGACGAGACAACTCTCCCCCACTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96	C T	GTTCAGTAA	...	GGGAGCCCTA GTTCAGTAA	TTTTTCAATTTTATCGGAATCCAGGACACAACTTCAGTAAACATACATATAGAAATTAACATTTG TCTCGGAATGGAGCCCTAGTTGACAGTAA/G/AGTGTATATAAATAATTCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37	C T	AATGGAA	...	GGCCTAAAGG AATGGAA	GCAAAAGCAAAAGCTATGGAGGCTAAAGGAATGGAA/G/AGTGTGGTGGTGGTGGTGGTGGT GCTTGTGTGCATGGAGAGAAAGTCTCTCTGCTCATGACGGGCGTCACATATTTTAAGTGCACATAAT TTGGCAAACTGTCTTC
WI-15153	40	A G	GCATGCA	...	CCCTTATGTTG GCATGCA	ATTTACAGTTGGCCAAAGATCTCCCTTATGTTGGCATTTGCA/G/AGACACTGCACATTTCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCTCTAA CCTTGTCTCTGAACTGGGACAGGATGTAATAATTTTGAATCTGTGAGGTCGAGGTATGGC TTTGAATCAAAATGGG/G/AGTGTCTTTTCCCTCTTGGTGGAAACCTCTGTGAGGGTTTGGCA
WI-15215	84	G C	TCAATGGG	...	CCCAAGGGGA AAAAGTCA	AGGAAAGAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGCACGACACTTGAGGAC CTAGAAAGCAAAAC/G/AGGAGTGAATTTAGCAATCAAAATGCAAGGTTGGAGATATGCTAAAA AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGGCTATGTAAGTACACAGTATGTCACACAC AGCCATGTGAGTGTACAGATCCCTCTGTGCAATTCAGCTTTCTTAAAAACATCAAAAGGCTGCA
WI-15152	51	G A	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGCACGACACTTGAGGAC CTAGAAAGCAAAAC/G/AGGAGTGAATTTAGCAATCAAAATGCAAGGTTGGAGATATGCTAAAA AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGGCTATGTAAGTACACAGTATGTCACACAC AGCCATGTGAGTGTACAGATCCCTCTGTGCAATTCAGCTTTCTTAAAAACATCAAAAGGCTGCA
WI-15123	55	C T	TAGGATG	...	TTGCTTAAGGG CAACAGAC	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGCACAGACAGATAAATAGGATG/C/AGTCTGTTT GCCCTTAAGCAATTTACAACTCAC.TGGGGAAGAAACAGACATGCAAAACAGAGATAAACACACAT

WI-15182	49 C A	GCACAACCCAG GGCAAAATA GGGCGCTTGGC	GCATGGGTTAA TCCAGCA ACTTATCCGTC	GAGACTGCCCTGTGACACAACCTAGCTAGCTGCACAACCCAGGGCAAAATAC/AJTGCTGGATTAAACCC ATGCTAATGGGTACCTTTATTTAGTAATCATGGGTCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	ACTATG CATTTATTGAG TATTCCTGCTT	AGGCAGAGTAG GTTGTAGTCTT ACATGCTTAAG	GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTC/TCTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTTT TCAAGTGGTAATAGCAATTTATGAGTATCTTCTGCTTTGATTC/TCTACTGTAAGCATGTAAAGACT ACAACATTACGACCCATCTCTTCAAGAGGAAGTCTGTTATTTATGAAAAACATTTTGTCTTCAGAT
WI-12601	42 T C	TGAT	TAGAC	T
WI-14510	104 A T	TGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATATGCCCTACATATTTAGTGTAAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATACAAAATAT/TGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	CATTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTTCATGGGAAAGATTGTGCAATTTGCAATAAACACCATCATTC/TCTCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTTCTCGCTGGGTGACGTTCCAGGCGAGT GAAGCCTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACTGTCTAGCAGTATTATTC/TCTGCTATTAGCTA TGTTTACAAATTTGCTCTGAAGGGGTCTAGATGTGTACACCCCGAGAAAGTGGTATTCCTGA
WI-15249	34 T C	GGGCTTGACAC AAAGTCTTAA AAGACACCGT	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTTTC/TCTGTTTAAATCTCTGGCTTTCTCTGGCTGG TGAGGAGGCACAGGCTGGGCTCTCAGGTATCCAGGTATCCACTGGTGGCCCGCATCTGTCTCCACTCCCGAG CCACATCTCTGGCTCT
WI-12159	28 C T	GCAATGTC	GTGCACTTT	CTGTCCGGGGAAGACACCGTGCAAATGCTC/TAAAGTGCACCTGAGGAGAGGGGAGGCTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGCGAGTTTCATCCACGGAGATCTGC
WI-12648	41 A	CCTAGTGCCAT GTAAGGATGC	TTGCTACTAAA AGTGGACATCC	TCCCCAGATTGTATGGAATGCTAGTGGCATTAAAGGATGC/TAGTAGGATGTCCACTTTTATGAGC AACCGATGTTAATTCACCTACTACTCTAGTGTGCTTTTACTTTGGATTATCTCACTTAAACCCACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGACAACAA AGCCTAAATGG	ATGAGAGGTAAAGTGTCAACAGTAAAGCTTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/G TCCATTATAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGAGGAAATTTAGCATAAATCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG	TCTCTCAGGG AGCTTGC	TTTATAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAAGCT AATCATGGA/TAGCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAAATGAGCTGGAGAAATTA TCTG
WI-15325	39 T C	CATGGCTGG GAGGC	CCITCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGGAGGCTTC/TTCACAATCATGGTGGGAAGGCAAAA GGCACACTTACATGGTGGCAGTCAAGAGAGAATGAGAGC
WI-13936	123 C T	AGTGGCATTC AATAGCCAT	TGAAACTCCCA CATGGATT	TATTTGAGTATTTTCATCCATGGGCTCTCACTCCCTATACATCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAAGACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATCTC/TAACTCCATGT GGGAGTTTTCATAATAA

WI-6375	28 A	GGTTATGCA TATGGAATC	AATGTGAGATC TTATTCTAAC CTTTT	AAGTTTATTGCATATGAAATCAATAG/AGTATCTTTTACAAAAAGGTTAGAATAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTTGTTTCTGATAAGACAAATCAAAATCAAT TACAACAATGTGCTTATCAGTCCCTCCACCCCTATATTTAAT/AGCAACTGACAGTTTGAAG GACACCAAGACAATAGGCT
WI-6409b	112 T A	TTGTGCTCAACAGATGAAATTCATAACCTTTGTTTCTGATAAGACAAATCAAAATCAAT TACAACAATGTGCTTATCAGTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGCT
WI-6409a	73 A T	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTCAATAGTTACTTAA CAGCTAAATAATAAGGGTGTATTAACTTACTTACAGAGTCACTAAATATGGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/TTTATCAACCTTCCCTAAGCATCTGTCTGTCCG CAGC
WI-6523	165 G T	GCTAATCCAGT AGAGACTGAA GCTG	AGATGCTTAGG GAAGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGGAAGTGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCTGTTCTCTCTTTTCACACAACCTTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACAGACAGCTAAACCTCTGAGAGAAAAC/G/GCTG ACTTTCAGAAAGCATAAAGCTGAGAAAA
WI-6554	195 C G	ATTGTAATTAATTTACATGGGCCTATTATTAAAGGACATTTGTGTAATGTTCCACTTTGTTTAAA /CT/TAATTACAACATGTGGCTTAAATATATGACAGATCAATGTAAACAGTTTGAAAAATGGCG
WI-6558b	68 C T	ATTGTAATTAATTTACATGGGCCTATTATTAAAGGACATTTGTGTAATGTTCCACTTTGTTT AAACAATTACAACATGTGGCTTAAATATATGACAGATCAATGTAAACAGTTTGAAAAATGGCG
WI-6558a	42 G C	AACCAACAAAACTAAGAAATGGGAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATAT/CGAAGCAATGGATGCTGTGTCAGAACATCTGCCAATAAAGCTTTAAGAAAAAGGA ACTCAATGAAGTTACTGTATATAAACAGGAGCTCACAGAGGGATGTAAAGATTATGGAAGAT ATCGTGAGCCAAAA
WI-6629	75 T C	TCTTTTCAGAG AATAAAAGTT GTGATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTTTCTCTGCTTTT TTACTTAGCAAAAGGAAACCTTAGTGAATGCTACTTGACACAGAAAGTCAATTTCTCAAGCACA T/C/ACCCAAACTTGAGGTGATTAAGCCCAATAATGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCCAAGCTATCTGGTTATTTTGTGTTGCTCAAT
WI-6644	134 T C	TGCTAAACACCACTTATTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAACAGT TGGGACGGTGGTAAAGGGCAGACACTCTGGAGCCACAGCTGTGGCTAATCACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	106 C T	CAGACTCTGG AGCCACAGC	TAGCC	

WI-6890a	28 T C A G A G	AAACACCACC ATTATTAAAGG	GCTGTGTTGG TAGTTTTCTCT	TGCTAAACACCACCATTATTAGGAGAGT/CJACTAGGAAAACCTACCAACACAGCATGTGAAAC AGTTGGCAGCGTGGTAAAGGGGACAGACTCTGGAGCCACAGCCGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAGCTGGTCTGTATTAACCAAGAGCGGTATCTGG
WI-6770	53 A G A A C A T C A C A	CAAAACCCAA G A A C A T C A C A	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTATGACACAGATCTTCCCAAAGTAATCCAAACCCAAACATCACA/GJAAATTATTCAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6886	151 A G A	GCATCTTCCA AAAACAAAGA	CCTTGTAAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAATCAGCTAGCACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTTCACTTTAAACATGGTAACTCCCAAGCATTTCT TCCAAAACAAAGAAAT/GJAACTTTGGAAATAGTCATTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG/CJACTCTTCCCTCCAGCTTTTGTGAACAAAC AATCTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTCCAGGTACAAGGTCTC
WI-6844	225 T C			TAAATACTGCCAACTAGCAATTACGCTCCACTTCGCATCATTTAAACAAAGGGTATTTCTCCTCTTG GTATTTCAATGATGCATTATACAAATAACGAAGTTAGAACTTTAAATGACCCCTGATTAATTAATG TAAACTGGTAATTTGTTTTTAAAGGCAATAAATTTGGTCTCTTCTCATAAAATGGAAATTTAAA TATTTCTCTGATAGTCTTGAGGT/CJATCATTATGATAGTGCAAAAGTGTG
WI-6824	112 A G			CGTTTCTGCTACACTTAATGGTTTTTTTTTAAAGGATTTTTTTCAGGTCTTGTGACGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCAAGAGTGTGCAAGAGTGTGCAAAATTTACAT GACACGGAGAAATGCGCTCTTGCTCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCAGAT CTTAGGAAGTGGCAAGTAAGGCAAAATCTTCTATCCCTTAGAGCTATTGTG
WI-6889	139 T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACCTTTGGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAAGAGCAACATGGAAGTGTCAAGAAACATCTGATAGGTACGGACAA AAGAGCTCTTCAATCAAGAGGAGTTACATATTAGTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCT/CJAGATAATTAAGGCCACAAAGTGAAGTGTGTTCTGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C			TCCCCAGCTCATATTTATTGGCAGAGTGGGCACCTCAATCTGATGAACCTTGATGAACCTGAA AAGAGGTCTCCTTAAACAGATATCATCTCCGAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAACTTTGCTTCCCAAGGAATGTGTTTCTAATTTGGTTTCAAGCAGACACTGGTTCC CACTTTTACCACCTT/CJATGACATTTGGACAAATAGTACTCTTTTCTAC
WI-9413	112 G C			GCCAGTCTCTAGTAAGTCTCTAGGACATGACACAGACAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACITGGGTGGAGGATACCGCTGTCTATTCGCCAGAT/GCJAGATTTGGTGGGAAGGAG ACCATGACAGATGACAAACGGAGACAGTTTCTCAAAAACAGAGGTATGA AAAAGCTTTAAAAAAAAGTGGTGCTATCTTTTGAACACACTTTCAGCAAGATCAAGTAGCCAGCT ACAGCCT/CJTTGGTGCATCTTAACCCCTCTCTCTTTT
WI-9557	74 C T			

WI-9617	37	G T	TGCTCTTTTATTTCACGTTTCACACACGCGTG(G/T)GGCACAGTCTACCAAGTGCCCGCAG CGCCACGCTTGGCCGGGAAGGTCTCTCTCTCTATGGACTGATGAAATTTGGGATGGCCAG CTCCAGAAATGCCACGTGGGGCAGCTCTGTGGCAGAGAGGCTGAGCCCTTGGCCACACTGGCACCA AAGAGGTTCACAGATGCAGCTTGCAGTGGGTCCAAAGCCGGTGCTGTG
WI-9657	121	T G	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTGCTGAAGTATAGCTACCATCCACTAT CATGAAATTTTGTCTTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT(G)ATAAATCTT TGTAATAAATAAATGTTTATAAATGTTTATGAAGCTCATACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G C	CCTGGGA	...	AAAAATTAAAC CAGGTGTGGTG T	CAGGCTTGCTCTGCTCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGGCTCAACCT CCTATGCTCAAGCCAGGCTCCCAAGTAGCTGGGACTCAGGCTGTG(C)ACACACACACCTGGTTAA TTTTTTTAAATTTTGTAAAGTAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACTAACTAAC CAGGCTTGCTCTGCTCTCCAGGCTAGAGTGAGTGAGTGACACAATCAAGACT(G)GACAGTAGCCCTCA ACCTCTATGCTCAAGCCAGGCTCCCAAGTAGCTGGGACTCAGGCTGTGACACACACACCTGGTTA ATTTTTTAAATTTTGTAAAGTAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACTAACTAA C
WI-13119a	51	C G	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT(C)CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACACTACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T	AGCTTTT	...	GGAAAAG	TGTTAACAATTTTATTTGGTAGCTCTCAGTACA(C)AAACACAGCATCAGTAGTGACACTTTTGAT AAAAAGAAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGCAAGATATAATGAATATGTACAT CTTTATGGAACCTGTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36	C A	CTCAGTACAA	...	CAAGGTGACA CTACTGATGCT GTTT	TGCTATTATGACAGACACAGTGGAGCAATATTCATTATACAGATGGAATAGAACCCAGACATTA TTTCACTACTTTAACCACTAATAGTGGAAACCTGTGAGACTTTAG(A)ATCTGCAAGGGTTTAAATAT GCAATATCACATATATTTCCATTTTACACCATATTTAAGTTTCCATTTTCTTAATAGAAAAATGA TAAAAATGTTTTCCCAATAT
WI-13020a	108	G A	CTTT	...	CAATTATAAC CCCTTTCAGA	TGTATAAAAATCCAACTTTTCCCAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCC(A)G/TACAAAAAAGCAAGCTTCTTCTATGGCCAGTTCTACAGAAGT AAGACTGTGCAAACTTTATGATAGTCAATGAGATTGCACACTAAGGCGAGGATGAGGCAAGCA AGTGTGTC
WI-12837	87	A G	AAAAGTCCA	...	GCCATAGGAA ATGCTGTTTTT	AGTGTGTC

L42611b	50 G C	GTCTCAGGCGCTTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCTGTGCTGCTCTCTGCGCTCTAG TCTTCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCT GCCCATCTGAGCACCCTTCTCACCATCAGATCAACCTTTGATTTACATCATATGATGATTACCA CTGGAGCTTCACTTTGTTAC
L42611	34 T C	GTCTCAGGCGCTTCTGGCTGCAGAGCCGCTTCTCTCAGGTTGCTGTGCTCTCTGCGCTCTAG TCTTCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCT GCCCATCTGAGCACCCTTCTCACCATCAGATCAACCTTTGATTTACATCATATGATGATTACCA CTGGAGCTTCACTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATGTTTGAATACCATTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTGAAGAAATGGCTGATACCAAGCTGCGAGTGAATAATGCA CATGATGAGCCTGGAACTGTGT TGAACGTGTGGTTAAAC/CATAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCTAGAAACAGTG GTGACCAACCTCAAGCAATGATTATCCCTAGCACTCAGATGTTTGAATACCATTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTGAAGAAATGGCTGATACCAAGCTGCGAGTGAATAATGCA CATGATGAGCCTGGAACTGTGT AGAGGCAGATTGGAAAGTGTGAAGAAATGAAAGAA/CJAAGAAAAAAGAGTCTAAATATTGAG AAATGTAAGTGTGCTCCCTCACTGTTCTTACCCACTTAATCTGCAATTTTGAAGAACTAGATTGAAT TCCCTTTCGAAAACCTTTCATCATGATACCCGAGTTAAACCGTTAATTAAGACATTAACATGCG CCTGGTG
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA GACTCTTT	TCCATGGTTGGTGTGCTACTGACTTTGTAGCCCTTACTGCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGGTGTTCAACAATAACACATAGGCTCTTTATCTCCTCTTTCAATATTTCTT TCACG/CATTAATCCCTCACCTGACCCCTTCTCCTTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231b	141 G A	TCCATGGTTGGTGTGCTACTGACTTTGTAGCCCTTACTGCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGGTGTTCAACAATAACACATAGGCTCTTTATCTCCTCTTTCAATATTTCTT TCACG/CATTAATCCCTCACCTGACCCCTGAAAGCCCTTCTCCTTCGTAGTGACATTTTAAATCCACTTTAC CACTTCGGACC
WI-1231a	126 T C A	GGCTCTTATT CTCCTCTCTTC AGGGAATAA	TCCATGGTTGGTGTGCTACTGACTTTGTAGCCCTTACTGCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGGTGTTCAACAATAACACATAGGCTCTTTATCTCCTCTTTCAATATTTCTT CTTTCACGTTATCCCTCACCTGACCCCTGAAAGCCCTTCTCCTTCGTAGTGACATTTTAAATCCACTTTAC CACTTCGGACC
WI-472	114 G C ACAGAAAAAG	ACATACATAT ICATTATACA GACCTTTCTTT TCCAGGCC	GAAAGGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATCTTTATTTTAAATTTTAT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG/CCTGGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAATGCAAGGCTGACAAATTTGGGCTTGAT

WI-478	46 C T T G T T C	GCATGCTGTG TTACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTTACTCTATTTGTTCTC/TAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTTAAAAATAAAAACCAAC ACTGCCCA
WI-533	29 T C A A C T	ATCAGAGCAG AGTACCTTTCT	CCITCCAACT CTACACAATCT T	AGCCATCAGCAGAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTCTGTGTATATGACCCCTGTGTCAGTTAATCCA
WI-601b	112 T A	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAAGCAGAGAGGTTTCACTTACTCTAACTGAGTAC/TJACAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG(C/T)GACAGAGAGGTTTCACTTACTCTAACTGAGTAC/TJACAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G C C T C A C C A	CTCCTTCACAA G C C T C A C C A	CTTCOCGGTAA GCCAAGT	AACAAAAACAGACACCCCTCGGCTCTCTCACCGATCCACATGGTGCCAAACATCCACACTTCCT ACATCTCCCACTGGGCTGCTCTTCCACAACTCACCAAGTACCTTACCGGGAAGCATATAA GCCAAAGCATTTAGTCTTTTATGCAACATGCTGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCCT GTTGATTTAAT	TTATCTAATC CCACATGACAG C	ACTCACTGCTTGTGTTGTTGATTATCAACCTAGCCQ/GJGCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAACACACAGATTGCTAACAAAGCAGATCTTTTTCAGGCACACGTAAAGAT AATAACTTCAA
WI-991	37 A T	TGCATTCAATTATGCACCAATAATACTCTGTACAT/TJTCATTATTGTATTTCATCACAAAAT TATGAGTGAGGATGATTGTATCCCTATTTACAGATGAGAACACACTGAGACTTGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTCCGAATCCATCACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACACACTGACTCTTTTCTCTCCITTTGAAAACAAGGC
WI-1011	70 G C C A	CAGTATCTGA AGTTTTGTCT	AGGAACACTA CAAAATGACTT CT	CTTCTGCACCTGTTGCAGTGGATGTTTGAAGGCTCTGCTCAAGTATCTGAAGTTTTTGTCTCC A/GCJGAAAGTCAATTTGTAGTGTTCTCTGGGCTTTTGTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGAGGCTTGCAGACATTTACAGATGGCTTTTGTCTGCAITCTGTGCACTGAAG TTTCATGCAGAGGTCATGATTTACAGAACTCAAGGAAGAGGCGCTGAGATGACACCCAGAA ATGAGAGTGGCTGCTCATGAAAATGGACAGCATGTTCCACAGAGGAGGACAGCATGGAGAAAG AAAAATCACTCTATCCCACTGCAGAACTGGCAATAGTTTGTJ/TJTTACTAAAACACAAATGT TTAACTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5381	178 A T	CTATGATTCCATCTAGCAAGCAAGACTATTTGGATAAGTTTCACAAAGATGAGAACAGGTCTCTA GAACCTCAG/GJATCGAAAGGAGTTTCATCTAGTCCATAGCCCTATCTCACTGACCCCAAGGTA AAAAAATAAAATAAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTTATTTTGGCCACCTGTTTGT TAGGAA
WI-5791b	76 G A	

WI-5791a	44 C G	CTATGATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTTC/GACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAGTTTCATCTAGTCCATAGACCCTATCTCAGTCCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCATTTCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T	CACTCTGCTGTGTCCATGGTGCCACAGACTCTTCCAGAAAGGCCACTTCCACAGATGCAACAGGCC TTTGAAGGAGCCCAAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTTATGAGCCAC ACTTCTATTCTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAGAGGCAAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	CACTCTGCTGTGTCCATGGTGCCACAGACTCTTCCAGAAAGGCCACTTCCACAGATGCAACAGGCC TTTGAAGGAGCCCAAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTTATGAGCCAC ACTTCTATTCTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAGAGGCAAA GG
WI-5406a	42 A G ...	TTTATCTCCC TTGTTTCTTT	CACTCTGCTGTGTCCATGGTGCCACAGACTCTTCCAGAAAGGCCACTTCCACAGATGCAACAGGCC TTTGAAGGAGCCCAAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTTATGAGCCAC ACTTCTATTCTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAGAGGCAAA GG
WI-5798	48 G C TG	ACTGTAGAAA ACCAGTATTT TCAAT	CCATTCTCTCTCCCTCTCCCTTATCTCCCTTGTCTTCTTGTG/C/ATTGAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACATATGTTAACAATGATGTTCTATATGGGTATCA
WI-5415	54 T A TTT	GGACTAAATCA TGATCCGATCT	CCTGCTAATAATAATTAAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT/TT/ATTAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTATCGAAATTGSA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAAGAG/C/TJCTTAAACCATATTTTGTGTTTA GAAACTCTGTGCCCACCACTCTGTGATGTGAGTGAC
WI-5481b	131 A G CTG CAGTGG	TTACTCCAGG CTCCAAGTAT	AAGCCAAATTCACATTAGTTGATGAATTTG/A/AAATTTACAGTATCTAAATGCAATGGCATCTGTTTC TCTCTGTTTTCAGAGGTTAGTATATGTCGAAAAATCTATTTTGTTCATTTATGCTGCAGTCGAA ATACTGGAGCCCTGGAAGTAAAGACTTGGCTATTTTTCACAAATTA
WI-5481a	29 G A AATT	CCCAATTCAC ATTAGTTGATG ATT	AAGCCAAATTCACATTAGTTGATGAATTTG/A/AAATTTACAGTATCTAAATGCAATGGCATCTGTTTC AATCTCTGTTTTCAGAGGTTAGTATATGTCGAAAAATCTATTTTGTTCATTTATGCTGCAGTCGAA ATACTGGAGCCCTGGAAGTAAAGACTTGGCTATTTTTCACAAATTA
WI-5492	38 T C	TCATGAGTCTTTCTTCAAGAGTGTGTTAAAGTCCCATCTG/C/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5865c	103 C G	TTAGAAACCTCCATTATCTGCCATGGTACATCTTTTAAAGATCTTTTTCATTATGCAATC ACTGACTCACTCACTGCTCTATCAAAATTAAAG/GAAATATTATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCCACAGTCTTCA GAGAAACAGACAACTAAATAATTCAGG
WI-5865b	99 T A	TTAGAAACCTCCATTATCTGCCATGGTACATCTTTTAAAGATCTTTTTCATTATGCAATC ACTGACTCACTCACTGCTCTATCAAAATTAAAGATCTTTTTCATTATGCAATC CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCCACAGTCTTCA GAGAAACAGACAACTAAATAATTCAGG
WI-5865	165 T A	TTAGAAACCTCCATTATCTGCCATGGTACATCTTTTAAAGATCTTTTTCATTATGCAATC ACTGACTCACTCACTGCTCTATCAAAATTAAAGATCTTTTTCATTATGCAATC AGAAGCCAGAAAAATGACCAAGACACAGTTCAGTCTCCATCTTCAAAAGGTCCACAGTCTTTC AGAGAAACAGACAACTAAATAATTCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTGG ATATGT	CTCAGACATTCATTATCTAGTTGTTAAATTTTGTGTATTTCTAGCATGGAATAATTATACAGAA AAAAATTTTGTACATATCAATGACTGAACCTTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTTCAGCCTCTCAGTTTTCATCTTCCATCTTTCATATTTTCTGTC ACAATGTTCTGCTCTGTTTCAACTCTCATCTGCTGATTGGATGGTATAGTATAAAATATGGGTGATTC AGAAAAATAGTAAATG
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG TTTTCATC	GACAGAAAAAG AGAGTAAATT ATGAAAAA	TTAGCAGAAACAAACAAAAATGTCACAACTGCACTGAAGAGTGTTCCTCCGATAAAATC/GIC CATTAGGTATTAGATAAGCATCCCATAAACATTTGTAACCAAGCGAGTTTTCGATTACACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATAGATAAGCGTCCACGAA CAITGTTGAAAAAGCCACGTTTCCGATTACACAGTTAGTTGCTGT
WI-5760b	61 C G	TTAGCAGAAACAAACAAAAATGTCACAACTGCACTGAAGAGTGTTCCTCCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTAACCAAGCGAGTTTTCGATTACACAGTT GTCGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA ACAATGTTGAAAAAGCCACGTTTTCGATTACACAGTTAGTTGCTGT
WI-5760	187 G A ...	TTCTCACCATG GGAATCTTG	GGGTGGATCT AACTTGCA	AAATCTGGCTTTTCTCTAGGAGGAGATTCTCACCATGGAATCTTGAGTGGCAAGTTAGAT CCACCTCTACTATTGAGAAGTAAAGTGAAGACTACTCATTTCTCAGTCTCTCTGCTG
WI-5944	52 A G GGAATCTTG	GAGTTTAATGAATCCTGTTCCCTCTAAACCTCTGTTCCCACTTCCACATTCAGCAGATTT CITTCATGGGTTATTTGCCCAAGTCATGAGAGATGATGATTTGATCATTTCAAGAGTGGAG TAAATGCTGGTAC/TTTGCTCTGTCGCGTATCTGCTCCATCAACCCATTCACCTTTTCTTATAT GCTGAATGAACGGTTATATTACAG
WI-5967b	148 C T	

WI-9720a	47 A G	CTCTAACAGAAACTTGACTTCCTCAACTCAAAATACCCTTCTCTAGJATAATTAAGTAACCA AAATAATCCTTCAAATAAATTAATCTTTTAATAGAGAAGCAACAGTGTTAGAGGTAGTACATTCA QCAC
WI-9825	123 A T	CACGCTAAGGCAGGATGGGCTTATGAGATACTTTGCATTGCTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCTTATGAGGATTAG TAAGATCTCTTTCTAAAGACAGAGAGATTATTTACAAGAAGAACTCACAGGGTTTATGTTGCATT TAAGAAITGCCAGTCTTTTGCTGCTGCAATCTTTGAACATAATACACATG
WI-9748	74 C G	CCACTTCAGTAAATCAATTTGTAGCAGTATTTCTAAAGATTTCTAATTTTATATATGTTACCCCTT GTCTATTCGTCAGACCAAGTACATGTTTTCACACAGCATCTTTCTCTCTGGAATCTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCA
WI-9943	91 T C	TGAGGCTATGATTGCAGATTGTAGTGACTAATACTTATTAGCAATTTCAATGTTGGGCACCTGT CGTTGGTTTATATCCATCTCTTCTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTGTCTCCTTATTTGTACCTTTAATATTGCATTTTCACACCTCTCTTTTGTCTATTAGGA
WI-9891	39 T C	AGGGGCTTCACAGATCCGTCAGCTCAACACTGCTCTCTTCTGAGTGAGCTGTGAACCCACCAAGAC GGCTGGTATCAGTGTCATCTCTCTCTTCCGGACAATCTTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCAATAATCTTTGTTTAAATCTCTTATAGGCCAATCCAA GTGCTGAAATATCTGCCAAGCATGCTCTACACAAAGGATTTGCAAA
WI-9897b	84 C T	CTCAGAAATTCAGATCTTCCCAATGTCTATCTTCTCAACATCTTATTTCTCTCAAC ATTTATCTAGCCTGTATCAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
WI-9897a	83 A T	CTCAGAAATTCAGATCTTCCCAATGTCTATCTTCTCAACATCTTATTTCTCTCAAC ATTTATCTAGCCTGTATCAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
WI-9935b	115 C A	AGATAACCCCTGGAAACTAGAGAAATTAATACGTGTTGTCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTCTTGGACTGGCAGGGGAGTTTCAGACATCAAGCAAGAAAGGCC TGATATTAGAGGGCACTTGCATTAA
WI-9935a	42 C T	AGATAACCCCTGGAAACTAGAGAAATTAATACGTGTTGTCACACCTCACAGAACTGGAAGGAGT AGTCTGACTGTGTTCTTATGGGGTCTTGGACTGGCAGGGGAGTTTCAGACATCAAGCAAGAAAGGCC TGATATTAGAGGGCACTTGCATTAA
WI-9983	146 C T	CTGTTAGGTGCGAGATCCATGCTCTTGGCCACAATTTAGGCTGCCCTCCCATTTCTTCTCTGA TTCCCAACCCCAAGTTCTACCCCAATCTGATCAATCTGACTAGGCTAGGCTGGTGCAGGGTAA AGCAATTATGATCACTAGACACAAAGAGAGGTTAAAGTTGCTGCTCTCAAGAGAGAGACATAA AAACAATGATCTGGAATAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10368	31	C T	TGAAGCAACC AGGCTCTGTT	CAAGATATTAT ATTATTCCT AAGAGGGG	GAGGAAGTGCCTGGAAGCAACAGGCTGTGTTCTACCCCTCTAGAGAATAAATAATATCTT GAGATAGGGAGGAGGAGCCCTGAGGACAGTCTGGGTTTGTCTACCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAATGCTGCTAACTATATGACCTGATGGATTGCTTTCAGGG T
WI-10391	32	A G	CTGCTCAGGT GTGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCCCGTCTCTGCTCAGGTATGACTCCCAAGTCAACTTCTGACTCCTAACCTCCCATCTCGGTG TCTGCTTCCAGGGGACGCTGCTGACACAGCTTTTGTCTGCTGTGACAAACAGAACTTGCAGAAAG TGATGCTGCGTGAACCTCCAGGATA
WI-10567c	146	A C	GTTAACCAGA GTCTCTAATA	TGCGGCTTCCA GTAGCT	AGGATGAATTTATATGTTATGCTGACTAGCGGGTCTCAATAAATAATATTTTTCATATT TTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATGCAAAACJAGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-10567b	82	A C	GGGTGCTCAAT AAATATTATT	... TAG	AGGATGAATTTATATGTTATGCTGACTAGCGGGTCTCAATAAATAATATTTTTCATATT TTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-10567a	60	T C	GGGTGCTCAAT AAATATTATT	AAATTCGTGTT GGTGAATAATTC TAG	AGGATGAATTTATATGTTATGCTGACTAGCGGGTCTCAATAAATAATATTTTTCATATT ATTTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-11153b	84	C G	CAAACITCAA ATTGCTTTAAG	AAATCCAACA GTCAAGGCTCT C	CGTTGGGAATTTCTATCTCACCTAAATTTATG/CAGTGAATTAATAATATACATTTTAACAACTTC TTGCTTTAAGTACTTTAC/GAGAGACCTTGACTGTGGATTTTGGATTTTCTTTTCTTTTCTTAATA AAACATGCTATATTAAGTTGTGAGCAAGATGACTTATATGTTAATTTCTGATATCAGCATCCCTT TATGTAAT
WI-11153a	33	A A	GGGAATTTTC TATCTCACCTA	GCAATTTGAAG TTTGTAAAT GTAT	CGTTGGGAATTTCTATCTCACCTAAATTTATG/CAGTGAATTAATAATATACATTTTAACAACTTC AAATTTGCTTTAAGTACTTTACGAGACCTTGACTGTGGATTTTGGATTTTCTTTTCTTTTCTTAATA AAACATGCTATATTAAGTTGTGAGCAAGATGACTTATATGTTAATTTCTGATATCAGCATCCCTT TATGTAAT
WI-2816	125	T C	CACAATGTA ACAAGAATTG	CCATGGCTGTA GTCCAGT ATCC	GTGTGAAATCCAGTATCATTTTCCCTCAAAACAGCTTAAATCAAAATCATTCTTTCTCTGTA GAGCTCAAACTCAGTCTGAATGAATTTGCTGCAAAATGTAACAAAGAAATGATCCTAT/CJACTGGG ACTACAGCCATGGAGAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C T	CAAGTGAATT ATGACCAAAA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAGGAACACACACAAAAAGTTTACCAGTGAATATGACCAAAATGAGAC/TAATAAT TTGTTAAAAAAACCTCAAAATGAAGAGAGACAAATATATAGTTCAAAAGATTCAGGTTCAATATTGT ACCTACAAATAGGGATAGTCAATGGTTTGGCAGACTTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTA GAAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCAATATTTTAAAGGAGAAATTCACCTTTTCT CTGTTGGATGATCAGAGTTCTGCTCTCTCCCAATCCAGAGGAGTACTATTCACCCCATGGGGTCTAT AGAGAGGATTAACACAGGGTGTGCTCTGCAATGGGAATATTGAAAAAC
WI-10656	59	T G

WI-11169b	154 T G	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCAITCA	CTGACTAGAGGCTGTAGTGACCTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACAT/GJTTCATCATGTGCTCTGATAAATTTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G	AATAAGTGAA AGTAACTGAC	AAACTCTGGT TAAAAAGCAC	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGCTCTGATAAATTTTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G	CAAGTCTGGACCTTGATAGGTC/GJACCGGGTGAAGGTTGGACAGTTGTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTTCCTTTGGGTTTACCACCTAGGGGTCACATAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGTCTCTAACTTTAATGGGCATA
WI-10686	133 C T	TGCCCCGTGTC AAGG	CAATCTCTAAA TTCATGTGTAG	AAATAACCTGTGGCACAATAAGGCAATACTGAGCCCCATACAGAGTGTTTTATGTTAATATTGAAA AAAGTCAAGAGAACAGATGATAGTTCTCTAGATACTTCTAGATACTTGAATCTGATGCCCTGTCCAAGG C/TJTGCTGTACACATGAATTTAGAGATTGAATGAATAATGGCAAAATTCAGAAAAAGGG
WI-11175	77 T A A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TTCCTTTTGAA	GGTAGGATGATTTAGAAATGCCACTTTACGCCACTGAATATAITGCCCTCCCAATGATCTTCTCG CTCAAAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTATTATCTGCTTTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAGTAAAGAAAAAGAGCCAATT TGCGC
WI-10694	144 A G	TGCAAAATGCTT TATATGATGTTTC	GGCATTITGTA AAGGAGGAA	TAGAGAGTCTTTCAGTTTCAGGGTTGGAGGGTGGTGAAGTGAAGTTCACCTTCTTGAAGCACTGGC TATGTACAGAAAGATAAAGTCTGAGAGAACTCAGTTCTAAAGTGTTCAGTCTTTCGCAATGCTTTA TGAGTTTTTGA/GJTTCCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGAGCTTTCT
WI-2716	23 T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTCTC TTC	T GTGAATTCATCCAGAAAAAGCTT/GJAAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCAGTGCATGGAGCAGTG
WI-10719	115 T C	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCACTCTGTCTAATAGTGTTTTAGAACACACACCTCAGTCAACAAAGTTTCTCTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAGTCTGGCTGGCAGTGCTT TTCAGCCTGCTGCCCATACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA GCTTGCCA	GAACTCCAC ATAAATAAT	CAACCAATTCAGATTAAATTTTGGCTCTGCTACTTGCCAAAGATGAGATTATTATGTGGGAGTT TCTGAAGATCCCATGGTAATAGTATCTCTCTCCCTGCTAGGTTTGAAGAGATTGAA

WI-11204b	88 T C ...	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTCACCTTTT/CATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-10732	80 C A ATGGTTCAC	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-11206	127 A T ACTC	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-11215	68 C T ...	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-11219b	89 G A AGAGAA	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-11219a	18 G A ...	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC
WI-11222b	136 G A GCCTGG	GTAAAAAGG TGAAAAAGAA	... TGATCACTTAA AATGTACATAA	GCACAGAAATGATTAAATATGGCTGACITTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAAACCTTT/CACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTAITCAGAAG GCAACATC

WI-11222a	25 C T A	GCCACAGTGG AATCAATTAC	TTTTAGCAATTT GCTGATTTG	AGCCACAGTGGAAATCATTTACACTATCTGAAATACAGCAAAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTTTTTCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACTGCGG CTGGGTGACAACTTGGCTACCAGGAGAACCTGACACAGACTTGTAAATGCTTTCACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATTATGCCATAATTAATTCATTACACTCTGACATCATATTTTCTTAGCAAAATACA TCTAGACACTGGCACTCAGTAAGGATATTCCTGGCACGATAATCATTTGTTTCAATTTAGCATTTGCA GGAAACCCATATGGATGATAATGTGTGTTTAAATGAAGGCAAGCAATTA TTGCATGCAATTTATACGAAAGGAATTAATATCTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAACAAAAAGTTTGAAGTATAGTAAACAAATGAATAGAAAAATGTCTCAGTGGTTGG TAGTACAGGAATCAAAATTTGGACTATGAACAATGACATAGTTGCTAAGGATATTCACACAAATTTAT TTCATGA
WI-11226	165 A C	GOAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC TTGAGGGACCC TGGA	CAGTGGCTGGTACTGACAAAAACGTAACTCGTGGCAGGTGGCAAGGGGTTGATCTGGAG TCCATCTGTGATGTACCCAGCAGGGCCAGGAAGGTTGATCTGGAG TGGGACACACTGCTCTAGACCTCTTCCAGGGTCCCTCAAAGGTGGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGAGCCAGAGGCATCAGGGCCCTTAGTCTCTCTGGGACAGTGAAGGGGCCACCAAC ACAGAAAAATGCTAGTCTTGTAGCAAGAGAGGAAAGCATCTTTCATGGGCGAGGAATTTCTCATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCTCTAGAAGTCATGCAAAAGAAATGATGA
WI-10810	58 C T GCAGGAAT	CATCTTCATGG GCAGGAAT	CAAAACCCTAAG AAACACAGAA ATG	GGACCAACAGAAATTAATCTGGCATCTGAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAGGATCAGGCTACCCAGGAATACAGTTAGGGAACATGTGGATGAATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATTTGGATACATTAGGCTATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATCTAA
WI-10828	23 T C			TATGCCCTCCCAACGAGCCATCCACGCTGCTTTAGCAAAAAAATAGAAATACATCATCTGAATG GGCATTAAATCTGCGAGCTCTGCTGCTTCTAAGTCCCTGCGTGTAGGTTGTCAGACACTGTGTGTA TACCATATAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAGGGCTGCTCGTGAATAC TAGTTGGG
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	A	GATTTGAGTATTAATAAAATGGCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAACATATA AAGAAATTAAGTGTCAAAGGTGTAAATCTTCTAATACCAATTTTATAGGGCCACCATTTAACTT CTGAAGAAAGGTGACATATGCAACTAAATTTCTAAAGTCCAGT
WI-10834	96 C T GTGTTAAT	AGAATTAAGT GTTCAAAGT	TGGCCCTATAA AATTGGTATTA AG	GGATGATGTTCTGTGGTCCCTTTATCTAAGGCTCTTGCATCCCAAAATGTGTAAATTTTATTTCT TGGTATTTCTGCTTAACCATAGTCACTGTCAAGTGTCTCCACCT
WI-2287	24 T C			

WI-2296	81 A G G A	TGTTACTTTGA TTCITTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGTCTCAGGCTTTAGAAATAAGTTGTTACTTTGA TTCITTTGCTCTGAC/GGCCAGTTAGCTGTGTGATTGCAAGAGTTACATTTGTTGTTG
WI-2300	77 G T C C A G T C A T A C	GGCACAAG CCAGTCATAC	GGTTGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCTTTATTTGAGCGGGGAGGTGTAGGCACAGAAGC CAGTCATAC/GTTTGCITTTAAATTTGACCAACCATTAACATAAGAAATAGCATTTCA
WI-2371	55 G T C C C A G C T C T	GTCTTGTTCTT CCAGCTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAAGGTCTGTGCTGTGACGTGTATAATCCAATCCTTGCCTCCAGCTTTACATGATGT GTCAATCTTTGACATTCCTTGTCTTGCAGCTGTATAATCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGGTGTCTGTG
WI-2395	122 A C T A C T A T C C A A	GAACATATT GTAGAAAAAT	TCACCTTTCTA TTTATCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAGAGTAACATAGAAATCATATAAATCTGGTTTAC TGAAATCTGAAACCTTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTCAAA/CJCTGAAATTC AGAATAATAGAAAGGTGAATCATCTTATATCAATTAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G A	CACCAGCCACCACCTACAACTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/G/AGCTGTG GTGCCAAGGACGCAATTAIG
WI-2437b	179 G A	CACCAGCCACCACCTACAACTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGAC/G/AAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTAIG
WI-2437a	128 G A	CACCAGCCACCACCTACAACTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATG/AJCTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTAIG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTATGTT	AACAACCTCTGC TATTTGCTCA C	CAGTAGGAACGGGTTCTCTCTTAGACCTCCAGAAAAATTAATGCAACCTACTGACAAATTAATTTA GTTG/G/AGTGAAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T C G A A A A A	TGTTTAGGAA ATAATGACAA	TGGTTACAACT GTACCAAAACAT G	CTGTAACCTACACACATCTCTCTGTAACTCTAGGTTACTTGTATACAAAAACACAATGTAAATGCT ACATAAATAATTGTCACTACTATATTTTGTAGGAATAATGACAAAGAAAAAGGCC/CJGTACAT GTTTGGTACAGTTGTAAACAGCCATTTTCCCAATATTTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C A G G A G A A G A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGCTGCAGCCCTGCAGAGTCTGGGGAGAAGAC/AAACGAGATAAAGCATG GCAAGACCAAGCTGAAAGTATCCAGGGTGTGTATGTGCAATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAGGTGTACAGAAAGACAGAGGAGCGTT

WI-2906b	77 T A ...	GACACCTTCAT	AGAGCAITCCA	...	CCTGAACACCTGGAGCACTTCCTCCCTGGACACCTTCATCTGCTGGAACTTTGCTGGAATGCTC
WI-2906a	50 A C TCTGCTGG	...	GGCAAGT	...	TTTCCCTCTTA/GAGCTTTGCTGGCTTACTTTTCTTTCTTTAGTTTACGCTTCAAAAGTGACCT
WI-1736	175 C T	CCTTAGAGTGGTTTGTGCTGACCAACAA
WI-1851	136 G A GTGTTAAGTA	CCTGAACACCTGGAGCACTTCCTCCCTGGACACCTTCATCTGCTGGACJACTTTGCTGGAAAT
WI-3000	62 G A AGACACAC	GCTCTTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGTTTTCAGCTTCAAAAGTGACCT
WI-1754	177 G A TAGTC	CCTTAGAGTGGTTTGTGCTGACCAACAA
WI-3167	37 T A TAGATC	TACTCCTCATCTCTCATGTCCCTAGACGTACAGATTCCATGCCCTGAACATTATTTCTTAAT
WI-3208	140 G A AGATAAAGA	TAGATTTCACACCCCGAGCACTATTACACAGAACAGCATGGAGCTTTGGAGTCTGGCTCTTAGA
WI-1775	47 C T TTTTCTCTG	GAACTTACTTAAGGACAGTGGTTTCCATCTGCTTCCA/CJTAGAGATCTAGGGTGTCTTTGGAACC
WI-3402	55 G A /ACAT	ACCTTGG
		AATACCCACGCTCTACACCAATCAGCTGATCATCAATCAGGTTTAACTATTAATCTGGGAGG
		ACACAAACATTTAGACCAATAGCAATTGAAITTAACCTAGATGTGTTAAGTAATTTAATCAATGGTA
		CA/G/AJACAACTCAGTTTAACTTGTAGTGAITTCATGTGGATACCATTCTTACATCATG
		TGA
		CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTGACGACCCCAACACAGAGACCCG/AJT
		GAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
		ATGGATCTGCTCAATTATAGTCCAGATAACAGCCCTCTCCCGGCCACCCCGGATTTATTTACT
		TAAGGGTTTAGCAAAITTCACCTGACGTAAGAGATTAGTTTCAACATGACCCCTCATAAAGTGATTTT
		TTCTCTTCTGTGTTTCTTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTGACCTTTCTGT
		AGCCACAAGATT
		ACAAACACAGCAAAATTAACCCACAGATCTATTAGATTCT/AJACCCATCTCAAAACTATCACATCAA
		AGAAGCAAGGAGACATATTACTGTGAGGAAGCCAAATTCAA
		CAAGCACACATTCAGGCGAGGTGAGGAGGAGGTGGGCAACTTGGCCAGCAGAGAGGAGGAAG
		AAGTTCAGACCGTTGGTAGGATAGTGGATCCAAACCCCTTTAGGGCAGGTGTGGAGTGGGCAG
		ATAAAG/AJCCAAAGCCCTAGTTTGTAGTGACACTGTGGGGATTCAAG
		ACTCCACCAACAGTTTGTGAGCCCAACCCCTGCA'TGGTCTTCTCTG/CJTJTACATCATTTGTCTATA
		AATCTCAACTGACATCATGCTCTGCGCAACCCCA
		CTGCCCTTTACATCCAAAGCAGATTACTCGAGCATATTCATTGATTTCCCTTACATG/AJCAAAATGCTC
		CTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCAACAAATAGATTTCCTTAGGA

WI-3416	33 C T	CCAA GTT GTA GCA T T CAG AA G T C	ACGAG CACAA CTA CCT CTAAG AG	TC TGG T T C C C A A G T T G A G C A T T C A G A A G T C T G T C T T A G A G G T A G T T G T G C T G C T G T T A A A A T A T G T T T T C A A G A T A G T A T C T C C C T G T T G T C A C T T C C T C C A A C A A G T G T A C C A A C A G C A T T G T T A A G G A A A T G T G C A A T G C T T G C T A C C T C T G A C G C A C A C A A T A A T T A A T C C C A T T G C C T A A A A G A C C A G G T C C T A T T C C T A C A C A C A G A A A T T T A C A A A T T G A A A T T G A A A T C A G C T A C T C T T C T T A G G C C C A T C A G A G A A T C / T G A A G T C A T G G G A A A T T G A T G C C A T G T G A A T T G G A A A C A G A C A C A G A C A G G C A T A T A T G G A G A A T T A C A G T T A C C A G G G A C A C A A T C C A C T T C C A G A G C C A T C A T C T G T A A A G A C C A T G C T A G G T A G A T C T G A T G A A G T T T G A C A C A A C T T A A A T C A T C A A G T G T G T C A A C T G G T T G A G T C A G T T T C C C T A A T T T T A G C A C A G T A T T T A T G A G G T G G T G T G G A A A A T T G A T G G T T G C G T A G T T G A G T T T C T G T C C A C C
WI-3453	70 C T	T T C T T A G C C C A T C A G A G A A	T C A A T T T T C C C C A T G A C T T C	A A T T C A G T T A C C A G G A C A C A A T C C A C T T C C A G A G C C A T C A T C T G T A A A G A C C A T G C T A G G T A G A T C T G A T G A A G T T T G A C A C A A C T T A A A T C A T C A A G T G T G T C A A C T G G T T G A G T C A G T T T C C C T A A T T T T A G C A C A G T A T T T A T G A G G T G G T G A T G G A A A A T T G A T G G T T G C G T A G T T G A G T T T C T G T C C A C C
WI-3474b	109 G A	AGT CAG T T T C C C T A A T T T T A G C A C	CA C C A T C A A T T T T C T C C A A	C A T G C T A G G T A G A T C T G A T C A T G A A G T T T G A C A A A C T T A A A T C A T C A A G T G T G T C A A C T G G T T G A G T C A G T T T C C C T A A T T T T A G C A C A G T A T T T A T G A G G T G G T G T G G A A A A T T G A T G G T T G C G T A G T T G A G T T T C T G T C C A C C
WI-3474a	90 A G	C C T G G G T T C T G G A T G T C T	G G G T G A C C C T G T C C T C A	T T T G A C C C A T A C A T G A G A A T A A A C C A T A A G A A A T G G T G G A A A A T A A A C G G G A G A C C T G G G T T T C T G G A T G T C T G T T G A G G A C A G G G T C A C C C C A C
WI-3502	79 C T	G G T T C T A A C C T G G A T A T A A A C A T C T	C C A G T G C A G C C T T C C A T	T C A C G G C A A G T T C T G C A G C A G T G T C C T T G A C T C C T G C C C T G T T T C C A G A G T C T G A T T A C C A T G C C C C T G A T A G T T C T G T G A G C C A C C T A A A C T C G T T T C C T G C T T A A G T T A T C C A G A G G T G G T T C T A A C C T G G A T A T A A A C A T C T G C A T G G A A G G C T G C A C T G G A T G A G G T C A C A A A
WI-3500b	146 G C	C C A T G C C C C T G G A T A G T T C T G	G G A A C G A G T T T A G G T G G C T C	T C A C G G C A A G T T C T G C A G C A G T G C C T T G A C T C C T G C C C T G T T T C C A G A G T C T G A T T A C C A T G C C C C T G A T A G T T C T G T G A G C C A C C T A A A C T C G T T T C C T G C T T A A G T T A T C C A G A G G T G G T T C T A A C C T G G A T A T A A A C A T C T G A T G G A A G G C T G C A C T G S A T G A G G T C A C A A A
WI-3600a	78 T G	C C A T G C C C C T G G A T A G T T C T G	G G A A C G A G T T T A G G T G G C T C	T A A A T C A T G C T T A T T T T C A C A A G G T A A T C C A C T C A C A A T A G G C A A T T G A T G A T C T C T T T C T G T A A G A A A A C T C T A C T C T C C T G A A C C C T T C T A C T G C C T G C C C T G T T A T G A T G C A C C T G T C C T T T T G G A T A G A T G G T T G A T A G G A G A T G G G T T A A A G A C A C A A T T A C C T T G T G T T T C A G G C A G A A A T A G A C T C T C T G T G A T A A C A C T G A T G A T T C C A A A G C C T T A T G T C T T A C
WI-3678	125 G T	A A A G C G A T T T G A G A T A C C A C A T C C A T G A A A A A G T A A A A C A C A C A C A C A C A A A A T A T G A C A T A A A A T A C A A A A A C T A C T A T A G T T T A T G A A A A T G A A A A T C C A A A A T C A G A G A A A A G T C A C T T A A A C A G G A T T C T C A T T C A T C C A G A T A C C T C T G T C A T T C T A A C T T T A A C T T T G A C T G C A C A G
WI-3687	67 A C	T C T A A A T G T A A C C A A A A A T C C T G A C A C A G C A C T A A C T G C C A G T C C T C A G T T A T G T A T C A A A T G A A A A A C T C A C A C C G G T T C A A T G A A A A A A A A A T G A T T G G T G A G C C A T G T C C C C T A T T A T T A A T G A A A A G A T C T T G G G C A A T T A A C T C
WI-3735	72 T C	C C T C A G T T A T G T A T C A A A T G A A A A A C	G G C T C A C C A A T C A T T G T T T T	

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WI-5204	54 C T	AGATAATTTTG TAAAGATAGTT TTGGC	TAGATTTTGATGACAAATAGGGAAGCCTTTGTTAAATTTGGGTTTGAAGAACTTGAAGAAAA TGAAGAGGGAAGAAATGACAGAAACCAAGAGAGTGTGAGGGGACGAAATCCAGTTTGACTGGA ATAAGAGGTGATGACGGTGG
WI-5215	70 A G C TCAAAA	TTGATCAAA GAGATGGGT GTTCTTT	AATTAAGAA ATCTTTACATG GTTCTTT	TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAA TAT/GJGCGAAACTATCTTTACAAAATATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCCT GTAGTCAAGGTTTAAAGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112 T G ATATA	AGTTGAATTA TTCAGAAAT TTATATGTC	TTGATCAAA GAGATGGGT GTTCTTT	CCCTGAAATGTCCTTGTCTCTCCACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTTAATTAACCTTGATCAAGAGATGGGTATATAAT/GJAAAGAACCATGTAAAGATTT CTTTAATTTAGTAAATTCATCAGGGCTCTCCACTGTCTATCAGTAA
WI-4456	49 C T TATATGCC	AGTTGAATTA TTCAGAAAT TTATATGTC	TTTCTGTTAT GCAATGAACCTG	ACACATTTTCATTTGCTTTAAGTTGAATTTATTCAGAAATTTATAGTTCC/GJCAAGTTTCATGCATAA CAGGAACACCCAGGTGGGCAATGATTTGAATGTT
WI-4461	49 A G CTTCC	TCATGTTAT TTAAATAT GCTTCC	TTGACCTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCAGCTGTTATTTTAAATTAATCTCTCC/GJTGAAATTTGGTGA GGTCAAGAAATGAATTCCTCCACTTTAGATTTCTGAAATTTATTTGCGATGATATATGCAATGGC CTACTGGATTTTACTTTGCTCAAGCCAGACAACAGATATATAAGAAACACAGTTAGTAACTCT TCACCTTTGATATTTCTCTTCTACTCAGGGAATC
WI-4465b	75 G A ...	GGTGAAGATT ACTAAGTGT TCCTT	GGTGAAGATT ACTAAGTGT TCCTT	CTACTGGAATTTACTTTGCTCAAGCCAGACAACACGAAAGT/GJATAAGAAAAACAGTTAGTAA CTTACCTTTGATTTCTCTTCTACTCAGGGAATC
WI-4465a	41 A G ACACGAAAGT	AAGCCAGACA ACACGAAAGT	AAGCCAGACA ACACGAAAGT	GGGTTAGGACCTCGAGATCTTTCAAGAACACATTCAAACCATATGCGAGTGCACAGGTAAACA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGCTGATGGTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCAATAATCTCTGTTGTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949b	160 T C TAATC	GGTGAAGATT ACTAAGTGT TCCTT	GGTGAAGATT ACTAAGTGT TCCTT	GGGTTAGGACCTCGAGATCTTTCAAGAACACATTCAAACCATATGCGAGTGCACAGGTAAACA GTGGTGAGATGCTCTGAGTTGCAAGGCTGCTGACATGCTGATGGTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCAATATCTCTGTTGTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G ATGCTGTAGT	CCATGTCACGA GCTTGTG	CCATGTCACGA GCTTGTG	GGGTTAGGACCTCGAGATCTTTCAAGAACACATTCAAACCATATGCGAGTGCACAGGTAAACA GTGGTGAGATGCTCTGAGTTGCAAGGCTGCTGACATGCTGATGGTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCAATATCTCTGTTGTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C AAGATG	TTCTAAAAATA ACACTTCTGA AAAA	TTCTAAAAATA ACACTTCTGA AAAA	TGAGAGAGTTTTTGATTATTCCTCTGCAACACTCCAAGTAAGTCTATCTATTCTGAAGATG/JC GAGTTCTCTTTTATATCTGATGATTTATTTTCAGGAAGTGTATTTTGAATAATAAACTCTGGGT CCATCCAGGCTAGGGTCAATGATCCATCCATGGGTGCTGGAGCAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACCATGTGG CATOC	GACAATGCAGC CATGCA	AGCTTTCTCTTTCTTAAAAATTTGGTGCCATAGTACTGGCTTCTGTGTCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTTGCATTAAGCAACCATGTGGCATOC/GTGTGATGGCTGCATTTGCCAGTC AAATGAGACAACCTTCTCTAT
WI-4582	226 T C	AGCAAGCATCTGGCAAGCCTGGTGACCAAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTTCAAGCCAGTTTAACTTTATTCCTGTACACA AATACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAAGACTCGGTTTGGCTGTACAAAGCAT AAACAGAACCGTTGCAAAATATGGTT/CCTCTCTAGAAACCAATTTGAT
WI-1965	105 G C	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAGGTAGTTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTTCAAGGG TAACCAACACCTTTTGGCCATTGAGGAAGTTTAAAG/GC/JAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTACAGT CATGG
WI-5248b	99 C T	CACTGTTTCT ATTGACCGTAC TTG	AGAAAAAGAG AAGAAAGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAAGGCCTAC CATTTTCACTGTTTCTTATAGCCGTACTG/C/TCTTTGCTTTTTCCTTCTCTCTCTCTCTCTG CCCTCTTTAACTAT
WI-5248a	38 G C	AGTTGTGCTG CTACGTTGT	TTTAAATTTG TGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAAGGCCTAC TACCATTTTCACTGTTTCTTATAGCCGTACTGCTCTTTTTCCTTCTCTCTCTCTCTCTG CCCTCTTTAACTAT
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGTGACTTTGCTCTGAAGCAGAAAGCAGCTGTGA CT/JACATTAATTAGCCCCATCTCTGCTGCTGAAGCCTGCTACAGCAATTTGTACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTGACAAAGATTCTCTTTTAAACA
WI-5252	119 A C	GAAATAGGGCAAAATTAAGACTTCAATTAATTAAGAAAGTCTTGGGAAAGGATTTGTGATGATCATG AATCTGTTTAAATACAGAAATTAATCTGAATACCTGTGTGAATCTGTTT/JCTACCATGTACA TATTATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G	GCAATGCTAG AAAAATTATGC CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATATGATAACCCAGGACTGTTTCAAGCAATGCTAGAAAAATTTATGCTA/JGJC CAAGTAGACAACTTAAGCAACAGGAGAAATGAAGTTTCTCTCTGTGCTAATTAAGTCTCTATCA ATTACCATTTATCGGGTAAATTAACACTGGAAAGTAAATGCCAGGCTAAATTTGTAGATTATGATAAT TACAGCTTTTGTATGCT
WI-5257	77 C A	GAGCATGAA GCAAGAGG	CCAGGGCAGA TGAAAG	CAATGAGAAGTTACCAAGTGGGCAAAATTAAGCATATGAAATACCAAGTTGTGGCAGAGGCATG AAGCAAAAGAGG/C/JCTTTTCACTGCCCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTTGCCTCC CGGATGAAAGATACCCCTCTATGACTACGCAATTCACCTCTAGGTATGCACCTTAACATATGGGTG GCAAAAT
WI-4649	50 C T	GAGACCATTTCT TTCCGAATG	TGTACTAGGTG TACTTACAGA AATCATC	TCAGTGTTTAGAAATTTCTTCTCTGCTGAGTGTGAGACCATCTTTCCGAATG/C/JGATGATTTCTGTGA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAGTACTTGTACCTGAATTTGTATTTTAA AAAAATCTCCCAATATG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGATGTTGTGTTGTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAGATATCTCAAGACATTTAATCTTAGAACCAAGAAAGTATAAGTTGTCTC TTATAITGCTTTT(A/G)CCAAATCCAGTTTAAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTGGAAAAATTTGCCAAAAAGTGATTGGTGAAAAAT GAGTTGAAATAAATG(T/C)AAGTTGAATAATGACACTGTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATTCGTAGAAAAATTTTACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGAAACTGCTTATCTTGATGTGTCAGTGACATTTCTTTTGTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCATCTG
WI-4722	88	G	A	TGCATATGG AACCCACAC	AATATGGAATC TGCAITTCAGTT G	CTTCCATTTGCCAGTTAGATGACTGCTCTCCACAGCCTAGAAAAAGATGGGAGATTATTTTC TGCATATGGAACACACACACG(A/C)CAACTGAATGCAGATTCCATATTGAATAGTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGAAAAATGGAGCCATGTACACAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTGAGTAAATCACTTTGATGGTTGAGATTTCAGAAAAAGTGAAATTTTGAAGTAACCATGGG TCAACTATGAT(C/A)CCAAACACAGCAGTGTGCTCTAAAAAATATGATAGTTCTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTT CCTGCTCATC	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGCACACAGAGGATTTGTGGCTTGCACAGGTTGTTGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGCGCTTCAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGCTCATG(T/C)TTAGGTAATTTGAGTTTCCAAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGATAGCTCCACATTCGCAGATTCAACCACTATGGATAGAAAAATAGTATTTCCAGATGG GCAGCCCAAGGATCAGAGGGCTAAATTTTAAATTTCCAAAGTTATACAGGACCAAGTTGGAAATTT AGCAATTTCTGGGTTTGGCATCCATCAGGGTGTAGAACTAATCCCTCAT(T/C)GAGAAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCCAGGCCCTCTCCACCATCTCCATCTCTACTCTGAT(T/C) AGGACACTTATATGGAATAAGGGA
WI-2034	150	T	C	CCACAGTGA CC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTTTTCAGAGTCCCTGGTACTCACAGAGAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTCTCGCGTTTCAGTGAAGAGAGATGAATCCTTCTATCTTACAGCAGCTGAGCTTCAACCA CAGTGCACCAAGGAGT(T/C)GGACCTGCAC(T)ATCTTTACCCCTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155 C T	TGTGCTTTAAAT GTGTGAAGT CA	ATTTCCTCTTG AAAGAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTCAATCACTACCATCTGCTGTTATTTGCTCTTCAGTG ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAACTGCTTTAAAGTGTGAAGTATTA ATTAGATTTCTATTTGATC/TJTGATGTTCTTTCAAGAGGAAATTTGTGAAGAGGATTCCTCATTT TGCATTTCCATTGGC
WI-4782	113 C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTC	TCATTGACTTTTATAGAGTTCTTCAGTCTTTATGCTTTATTTCTTAGGAAAACTAGGCTAGGAGAA CACAAATCAGGTTCTCCAGATGCAGAGATACTAGAAAAATGCTJTGAAACAGAAAAATAACCA GAAGAGTTCAATTATGGTTTCTTTTCCAGAACGATTAC
WI-4788	65 A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAAATCATCTTCTGTAAGTCCJAG JTGAAAAAAATATGCCAAAAATTTAAATTTATCCAAACTTTAAGTCGAGATTATAATGTATATTT AAAAAACTATATGAGTCTTTCTTAAAGATGGCGTATCACTCTA
WI-5300	38 T C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTTCTATAATC CAAAAA	CTTACTTCCAAAGTGTTTTCCAGAGACCACTTCTTCTTCTTGGATTGAATGAATGAAGAGAT AGGTGTTATTTCTCTCTTTTACCAGGTGAAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGCAGAGGCCA
WI-4818b	121 G T	TGATAATGGG GCCCTGTT GA	CCTCCCTTTA TATGTATGCCA GA	TATAATGTTTGTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAACAATCTTATATA ATAATTTATCAAGAGGAAATATACATATGGGGTGATTAATGGGGCCCTGTJG/TJCTCTGGCATA CATATAAAGGGAAGGCTAA
WI-4818a	43 A G C	TTGCCATAGAC TAGGTATATGC AATAAAT	CATATGTATAT TTTCTCTCTTG AATAAAT	TATAATGTTTGTCCATAGTTGCCATAGACTAGGTTATGTCCJAGACATGAATAACAATCTTAT ATAATAATTTATCAAGAGGAAATATACATATGGGGTGATTAATGGGGCCCTGTGCTCTGGCATA CATATAAAGGGAAGGCTAA
WI-5317	139 T C	TTCCATTCTG GTAGCAGGT C	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATAATAATATGATGTTATATATACAAATTTCAACTCAACAGGAAATTCATTTCTGTAGCAGGT ATA/TCTGGACTCATTTCTCTTTCATCTATTTCTAGGTTATTTGCAGCCCGAGATCTACCCAGG
WI-4888	56 G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCACCTA CCTCATTTATT CA	AAATGAGTAACCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA/GA/JATGAAT AAATGAGGTAGTGAATTTGTTGATACTGGAGTAGTGCCTT
WI-5328	44 A G	AACATTTTTAACCTGCTACATTTACAAACACTGAAAGACAGJAG/JAAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATCTGGAAGGAG
WI-4897	93 A G	GCTTTTTGAGTTTAACTCTTTTGTAGTGTCTTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAAAGAAATAAGCGCTTGGJAG/JATAAACAATCTTC
WI-5345	29 G A	CCCTGCTATAGTGCAGTTTAAAAATCCCTG/JA/CCTGCTATGGTTGCTTGTGTTGAAGCCACATCCACT GAGGTATATTCTGCTGCAATTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGACAG

WI-5370	143	T C A T A A A C A A	A A A	A A T A A G A T G G T A C C T T A A C T A	C A A A G T T G G T A C A G A G A A T T T C	T G C A T G T T A C T T C T T G A A A T C A T A A G G G A C T G A G A G C C T A C A G T A T A T G G C A A C A T T A A C C A A T C T T T T G A A A T T A C C T G T A T C C C A T C A T G G T T C A T T G C A A A A A A A T A A G A T G T A C C T T T A A C T A A T A A A C A A T C T T T G A A A T T C T C T G T A C C A C T T T G C T T T C G A T C C C T C A T C C C T C C A G A A G A G A G A A G A A C A C A A G A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G G A T G T G A A T G C C C A G G T G A G G A C G G C T T G C T G A T G T G G G A A A G C A C T G A C C T C A C A G T T G G A A A T G T T G T A G T T A G C T G C T G A T C C T G A A G C T T G C A G C A G C T T C A G T T T C T G C C C T G T G G A A A T A T T T C C C T G A T A C T C T A A A A T T T G A A T G G A T C C C T C A T C C C T C C A G A A G A G A G A A G A A C A C A A G A A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G A T G A A T G C C C A G G T G A G G A G A C G G C T T G C T G A T G G G A A A G C A C T G G A C C T C A C A G T T G G A A A T G T T G A G T T A G C T G C T G A T C C T T G A A G C T T G A A G C T T G C A G C A G C T T C A G T T T C T G C C C T G T G G A A A T A T T T C C C T G A T A C T C T A A A A T T T G A A T G G A G A A T T T C A G G T G A A T G G A C T G C C C C C T C C T G A T C A C T G C T A C C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T C T C A G T T T A T T C T A A C T T A A T G A T C T C T G A C T T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C G A T A G G G A G A A T T C A G G T G A A T G G A C T G C C C C C T C C C C T C C T G A T C A C T G C T A C C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C C T C T G C C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C C A G T T T C A G T T T A T T C T A A C T T A A T G A T C T C T G A C T T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C G A T A G G G A G A A T T C A G G T G A A T G G A C T G C C C C C T C C C C T C C T G A T C A C T G C T A C C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C C T C T G C C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C C A G T T T C A G T T T A T T C T A A C T T A A T G A T C T C T G A C T T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C G A T A G G G A G A A T T C A G G T G A A T G G A C T G C C C C C T C C C C T C C T G A T C A C T G C T A C C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C C T C T G C C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C C A G T T T C A G T T T A T T C T A A C T T A A T G A T C T C T G A C T T C T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C G T A T A G T A T T A A C A A G C C T A G A A G C A G G C T G T G G G T G G T A T T T G G T C A A G C A T A T C T A G G T A T A T A A C T T T G A A G C C A A C T T T A A C T G G A G T G G T T G A T T C T T T T T A A T T T T A T T T T G G G A G G G T T G G A T T T A A C T T T T T T A A T G T T G T T A A T A T T A A G T T T T G T A A A G G A A A C C A C T C T G T G A T T A C C T C A A T C A T T T G T A G A A T G G C T A C T A T C A T G G C A G A G C A G C C A C T T T T G G T A A T T T A C A T C C A A G C T A A T A A T A A T C A A G A A A A T A G A G A A C A T T A A C A A A A T A A A T A T G T T C T A T T T G G A A T A C C T A A T A T C A G A T A C T A A C A A G T A C A G T A A A G A A T A A A A A G A T A A T A A T C A C A C A C A C A C C T T C T A G G T T A G T A G A A A A G C T G T C T C T A G G T T A G T A G A A A G T T
WI-971b	423	T A
WI-9711a	390	C A
WI-9702c	345	G A
WI-9702b	344	C T
WI-9702a	179	C T
TGR- A003N21	49	C A
TGR- A004V30	203	C T

WI-7593	46 G A	TTTGTGTTGCTCTGGACACCCACTGCTCCAGGATGAAGAGAG(G)AATGAGATCATGTTTGGACATTTCTCTCTCTGAAATCAACAGITACAGTCACTGTTGGGACTCTCTCTCTCTCAA
WI-6962	78 A G	AGTGCATCTGGGGGAAAGGCTCCAGTGTATCTGGACAGTCTCTTATTTTCAGGTGGGACTCTTGATCCAGAG(A)GACAAAGCTCTCAGAGCTGGTGTATATCAAGACAGAACCCAAAGTCTCCGTCTGGCTCTATGCTCTATCTCTATCATAGATACATCTCCACAGCTCACTTCACTTCCAGCTATCTCTGAAAATATCTCCCTGAGAGAACAGAGATTTAGATAAGA
WI-7059	43 C G ...	GGTCA	GCATGAGAGAACCATCGCCAGGGGAGAGCCACCCAGCCATC(G)TGACCCAGCGAGGAGCCAACTATCCCAAAATATACCTGGGTGAAATATACCAAATCTCGCATCTCCAGAGGAAATAAAGAAATAAAGATGAATGTTGCAACTCTTAAAAA
WI-9063	53 A C TT	CTACTTTCTG COCTTGGGT	AGCAGCCATCACATGATCTGTTTTTCCACACTTCACTGAAAGACACCATTTATATCJTACCCAAAGGCAGAAAGTAGAACTTACTTATCTAATGTTTGACACAAATGGAAATGTG
WI-7079	293 T G ...	GACAGATTTT GACCTAGTTCC TT	AAGGGCATTTGAGACTATAAGCAGTAGACAATCCCACTACCATCTGTAGAGTTTGGAACTGCAATCTTTTAAAGTTTATATGATATTTTAGGGCTGCTAGACTTACTTCTCTATTTCTTTTCCATTTGCTTATCTTGAGCACAAATGATAATCAATATATACATATACATCACTTTTGTGACTTTTTCCTCAAGCCCTTTTACAGCTTGGCATTTTCTCGCTAGGCTGTGAGGTAACTTGGGAT
WI-9074	38 A G AAAAG	GGTAAAAGTT CTTTTGTCT	TGGATGCGGAGGTAAAGTCTTTTCTCTAAAAGAG(A)GAGGAAGTGTGCAAAATCTGTCTGTTGACCTATCAGTTATTAATTTTAAAGGATGTGCACTGGCAATGTAACTGT
WI-7104b	249 C T	GGAGTTTGCCCTTCTAAGGGAAGGAGATCTTATCTTTCTGTTGGTGTGACCATCAGTCTGGGAAGAGAGAGAGTGCAGAGAACCTGAGGAGCCGGTCTACTTTGCACTGAGAGAGGAGGCCCAAGCTGTGAGAGACATAGGCCAGCAAGAGGGCTTGGTCTGAGGAGCAGATGTTTCATGCTGTGAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTGGCTT
WI-7104	157 C A ...	TGTAGGGCTGA GCTTGGC	GGAGTTTGCCCTTCTAAGGGAAGGAGATCTTATCTTTCTGTTGGTGTGACCATCAGTCTGGGAAGAGAGAGAGTGCAGAGAACCTGAGGAGCCGGTCTACTTTGCACTGAGAGAGGAGGCCCAAGCTGTGAGAGACATAGGCCAGCAAGAGGGCTTGGTCTGAGGAGCAGATGTTTCATGCTGTGAGGCCCTTGACAGAGGTGGGGCCACAGCCAGCAGCATCTTGGCT
WI-8974	34 C T AAGAACTCA	GCTTACAGGAG GACTTAGACA AGAA	CATACAATTGAGAGCCCTGAGCCCTCAAGAACTCACTGCAAGCTCAGCCCTACACAGTTTCCAGCTGGAGTTTCATGCAAGGCCAAAAGGAGTGCCTATGCAAGCTGTTTAA
WI-9161	61 C T CTTGGC	...	CTGTGAGGGTGAAGTTAGCATTACCCCAACCTCATTTTAGTTGCTTAMSCATGCTGGC(C)TTTCTGTCTAGTCTCTCTGTAGCCCAAGAAATGAACATCCA
WI-9014c	93 T C	COCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCACTTCTCTGTTCCAGAGGTGGGGCTGGATGTCCTCATCTCTGTCTCAACTTTATGCTGTGAC(T)GAGCTGCAACTCT

WI-9231	32 GC	CAGTCCCCCA GATTGA	CACITGCCAC ACTCAGAC	GTGACCTGTGAGGTCCCGCAGATTGAGCTGTGAGTGTGGCAAGTGTGTCAAAAGGGGCG TGCCCCCAGGAGATGAGGCTGAGAGGAGGAGTGGAGCCGAGAGTCA
WI-7836	120 T C C	CAATAAACA ATGCAACGTTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGATTGAGATAACACTCTCATTCAGTAGTTACTGAAAGAAAACCTCTGCTA GAATGATAAATGTCATGGTGTCTATAACTCCAAATAAACAATGCAACGTTCCCT/CJGATTCTTAAT CTTGGTTCTGAGAGCCATTGGTTTTCAGTTGTAGCAATCCCATACAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAAGTACAG TAA	AAACAACTTA ACCAGAAAGCT TTAA	TCCATTCCTTTTGGCCCTGCAGCATGTCTGTCCTCCAGAAATTCAGCTTCAGCTTAACCTGACAGATTC GTTAAAGCTTTTCTGGTTAGATTGTTTTCATCTGGTGATGATGCTCTTTTCCATGTGTACCTGTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	GTAAAGCATGT ACGTGAATTTT T	CCCAATTTTAA TTAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAAAATGTTAAATAACAATATGAATTTTCTCATGTCATATTAATACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAACATTTTAAATAAATTTGGGGTGTGG GAAATTAAGGGAGGGTGTCTCTGTGGTCTCCCTCCCTGCCCCCA/CAGTGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGAACCTTGACCACTACTGGCCCTATGGGTTGGGGTGTGTAGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAAAGTGTACTTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGTCTCTCTAGGAGGAAACAGGAGACCTGGGGTCTCTGGAT
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGA AGTCTCGCAGA	CAAGGGTACCTCCAAACATAATTGATTCTGATCTGCGAGACTTACACTAAGCAATCCTGAGG AATAGTGGAGGAGGCGCTGGCTACTGTCTCTGCACTCTGCTGCTTTG CACACTTGTCTTCTTTCAGTGTGGAGTCTCTGGAGGTCAGGCTGGGGTAAGCCGGGGTTCCACA GGCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGCGGAGAGCACTCCCTCCCTCAGTGTAACT GGAGGAGGGAGCTCCAGGAATGGGAAATGTGACACCAACCATCTCTGAAAGCCAGCTTCCACCTCCAGT TTGCACAGGGGATTGTCTGGGGGCTGAGGGCCCTGTCCCAACCCCGGCG
WI-7307	128 G T	GAAATGTGAC TTCACITTTGGT T	CAGGTAGAATT TCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTGCTCAATGGACAGAAATCTACCTGTGTACATAGGAGAA GTTTGGAAATGCACATAATAGCTGTTTACACCTTGATTTCGAGGTGGAAA AATCCCTTTCTGGTAATCAGGCACATGATGAATTTGATTAGTAGGCTGTGATTAAAGTCTTTAAAT TGTTTGCAGTCTTTTATGTTTATCATAGGTATAGGTAGGAGCTAAATTCCTTATCATATCTTTAT AATCAGCCAGTGTATCCACCACTTTTGTATGTTTAAAGTAACTTATCTCTGGATTTCATG AAGGTGAATATCGTTTGTAAACTGAATAGAAATGTATAGCGATGA
WI-9274	25 C T G			AATCCCTTTCTGGTAATCAGGCACATGATGAATTTGATTAGTAGGCTGTGATTAAAGTCTTTAAAT TGTTTGCAGTCTTTTATGTTTATCATAGGTATAGGTAGGAGCTAAATTCCTTATCATATCTTTAT AATCAGCCAGTGTATCCACCACTTTTGTATGTTTAAAGTAACTTATCTCTGGATTTCATG AAGGTGAATATCGTTTGTAAACTGAATAGAAATGTATAGCGATGA
WI-7313e	266 T C			
WI-7313c	256 C T			

WI-9281	68 GA ...	GCTAACACTTT TTAAACCGT	CAITTAITTTG AAAGCTATTCA GACA	...	ACTGGTGGAGACTGTGGATCCAGGATTCTGATTTCTGGCCAGAGGGCTTGCTGGCTACTGG (GAT)GTAGTTTGACAGTCTGGTGTCTCCCTCTCTTAAGACTGTGTCC
WI-7848	142 A G CTC	GTATTACA ATGATCACCG	CCACACGAAC TATTGTAACAC AA	...	TTCTGAAATATAACACGCCATTGAGCTATTAAACCTGTAAATTTTTTAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACATAAACAATTAATGCTAACACTTTTTTAA ACCGTCTCAGTGCTGCTGAATAGCTTTCAAATAAATGTGAAATGGT
WI-9304	70 GA ACTGA	GTATTACA ATGATCACCG	CCACACGAAC TATTGTAACAC AA	...	TCACGTTGGTGTCTCAGATTCTGAGGAAATGCTTTGTATTGTATATACAATGATCACCGACT GAG(A)AATATTGTTTACAATGTTCTGGGGCTGTTTTTGT
WI-7933b	314 C A	TTACAGAACTTGCCTGTGCTGTCGCCCTGTCGCCCTGCTAGGGCGGAGGGGTCTTTCTCTCTCTTCC TACCTACCCCTTTCTCTGGCCAGGGCTCGATCTCTACCTTCTTCCCTGGCTGGCTGGCTGAC CACAGAGATTGCCCTTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCA AGAGATTGCCCTTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCA AGTTAAGGGACCATGGCTGGCTGGTGGGAGGAACCATAGCTCCT
WI-7933	96 GC	TTACAGAACTTGCCTGTGCTGTCGCCCTGCTAGGGCGGAGGGGTCTTTCTCTCTCTTCTTCC TACCTACCCCTTTCTCTGGCCAGGGCTCGATCTCTACCTTCTTCCCTGGCTGGCTGGCTGAC CACAGAGATTGCCCTTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCA CAAAGTCTAAGGGACCATGGCTGGCTGGTGGGAGGAACCATAGCT
WI-7374	182 T A	CCAGATGTGCCATCAGCTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAA CCATGGTGAGAAAGTTTGACTTTGTAAATAATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGGAAGAAATATTTG(A)CAGAAACACAAAGGCTT GAT
WI-9343	78 C T CCTCTGCCA	CCACAACAT TCTCTGCCA	AAATGAACCTT ACGTTTGTG TG	...	GGTGTCTCTGCTACTGACCTTCCCTTCCCTGCTCTCTCATCATCATCTCCCAACAACAT CCTCTGCCA(C)TACACAACAAACGTAGTTTCATTTGGGCAA
WI-7386b	104 T A	CTATATGTAGAGCGGTGATCTGGATGGAAGTTGGCTGGATGATCTCCAAGTGTTCGAACCTCT TAAAGACATCTTAATCCCTGAATGTAAACAAATTTGTTA(T)A/IGTGTTTAGAATCAGAATTTGATTTTGA ACTTGAGTAATTCCTCT
WI-9357	75 A G ...	CTTTAGAAAA TCTGCTTTAAC	AAGAAGGACTCAGTTACGGGGTTTTAAACCCTCATGAAACCTCGAAGAGTTCACTTTTGTATTAT GCTCT(A)A/IGTATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79 T C TTGG	CTTTAGAAAA TCTGCTTTAAC	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGGAACCACTACTTTAGAAAACTGTG CTTTAACTTGGT(C)ATTCCTCTAAATTTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107 T C GTTC	TGCTGGGCTGT	GGTCCAGAAGA GGGG	...	TGCTCCCTGTCCACTCTGCAGTGGACCCAGCAACCCCTTTGAGAGGTGGGTGAAGTCTGCTCTT GGCAGGATTTGTGACACTGCATTGCTGGGTGTGTTCTGCTGGGCTCTTCTGCACTTGCACCGTG GATACCAGGCCATGTGCCATGTATTGGTCTGGGAGGGTGGGTGAAATAAGGCATCTGCTCT

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGAGGGAGAGAGCAAGATTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCAACCTAGAAACGTTTCATTGTCATTCACAGAGAGAGAGGAAAGAAAAA [T/A]ACAACTTTCATCTCTTTTGACACGTTTCATAAACATCTACATA TCCTGCAAGAAGTCTCAAGCCCTTTTGATTTTGTGCAATAAGTACAGCTTTGCATAAGAGTGAAA TTGGCTAGCTTAATGATGATCCATAAATCTCTCTAATTTTAAAGTGAG[A/C]TCTTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAAAATTATGTACCACCTGTTTATTGTTCATCATCCA TCCCTTTTCCCATGAATATTTCA GTGGCCACTACATGTTATAGAAACCATCATCTTTGTACACAGCAGCAGTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAGAGTGTCCCATTAAGAGGAGCTTTTAAATCAACCTAA TAACTCTAATTCGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAGGGTCACA ATTAATCTTTGATCTTTTACTCAGTGTAACTTATATAAT[A/T]TCAGAAC TACACAATGAATTCCTTTTATTTGGGTATGCATCCACATTTACAGCATTTAGTGGTCTGCAACAGCAAG TGGAAGACGAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCGG GTTCTCTTAATCCCTGCTGAGGATCTTTG[A]GAAGCAGCAGCAGCACCACCAAGGCGATGCA COGGATTCAAGGTTCTTTTGTCCAGTTGTACAGATCCAAACTAGACCCCA AACAGTCAACCAACACATGACAACTCGCCAGGCAAGGCTTCTCCCTCCCTCTTTCGCTGCC ATGTGCTAGTCAGCAAGGTGCGGGAGGCAACGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA[A/G]GGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCATTAAAACTG ATTGCTTTCAGTAACTGGTATGCTGAA ACCAAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGTTGTTGGCTTCTGAAAGAAACCTTGC TGACAGCTCTCACTGACCTGACGACGAGGAAACCGTACCTGAGAGGGGATGGGGCTCTCTCAGAAA GAATTTTGGGGCAGAACCTGGAACCTGGCCACGAGGACATCCCAATATCCCTCTCTCTCAGGG CTCACCCGACATCTCAGCCAAATGAAGGCTCTGAA GGGTGAGACGGGTTTATTGTGCACATTTACAGCGGTCAAGCTGTGGGCTGGCAGCGGCCATGCTC CTGTGTCGGGCTGCTACAAAGGGCTTCACTTTTCTCACCACATGTACAGTCAGTGTGCTCCAA GGTATGGGCTACAGTCTGCATCAGTGAGTCTGTACACACATTTTACATAAATTACACAGACTC ATACATGAAAA[A/T]AAGAGCCTAAGGGCTGTATTTAATGAGAAAAA AACTGTTTACAAAAAGGCTTTGCAAACTTCACTACTGAATTTGAAAGTCAATGACTGTGTTGTTT TAAATAATGTACCAAGGAATACAAATTTGGATAATGATCATTTTTCATGCTCAGGAGAAACAGCAG AGAAATAAGGATACGCAAGGTGCAAGGAAACCGGAAACCCATTTGTGACTGTCTTCACACAG [G/A]GCATCTCTTCTACCTTAACTGCAGCTGTGCAAGATGCTCAGTGTG
X86400	118 A C
WI-8053	242 T A
WI-6190	165 G A
WI-6275	148 G C
WI-6421	41 G T
WI-6905	215 T A
WI-9420	202 G A

WI-9448	184 GA	---	---	TGGGGCTGCTTTTAGACITTCATTTCTAGACGACGACCACTAGTGAGAGGAATACCTGGAGAGAGAC TGCCCTTGCCCATGGTGGTTAAOCTACATAGGGGACTGAAATCTCTTGATGCGCAGTGACATGCC TTTTAGAAAAATGGCTTGTTGTTCCAAAGCTGAGAGCTGGCAACAQ(G/A)CACTGGTTCTTAA TCTTGCTTGATTTATCCAAGCGCATGTTCTAACGTGCGCTGGAG
WI-9470	204 GA	---	---	ATGTCAGAGAGACACAGACAGAGGATTTTCCCTTTTAATGCTAAACAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCCAGGTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCGCTTA TGATATCAGAAATATGATCTCCCTAAAGCCAGATTCTCTACTAGACGCGCTGGGACACTGATGAC AA(G/A)GCAATCACTCATCTCTAAGCTCACAGGGCTCACCTTCCCAAG
WI-1245b	201 GT	---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCAAGCCCTATAAGGAAGATGAGGTGTTAATGGCA TCTTAGGGCAATGGTAGTGCTGATGCAGATCTGCTGTGAGCCATGCTGGCATCACAGGGTGGT TATTAATTTTATATCATCTGGACAGCCCTTCTTAAAGTACATCCTTGCTCTCTCTGAGGCG TCTAAGTCCCAAGGTGGCTCTGTATCCAGAA
WI-1245a	85 TC	---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCAAGCCCTATAAGGAAGATGAGGTGTTAATGGCA TCTTAGGGCAATGGTAGTGCTGATGCAGATCTGCTGTGAGCCATGCTGGCATCACAGGGTGGT GGTTTATTAATTTCAATTATCATCTGGACAGCCCTTCTTAAAGTACATCCTTGCTCTCTCTGAGGCG GCTAAGTCCCAAGGTGGCTCTGTATCCAGAA
WI-1031	149 GA	---	---	TTCAAGTAAAGGACAGGTCTAGAACAAAGGCTTCCCAACCCCTGGCACCATAAGACATTTGGACCAA TAACTCTTTTTCAGGGGACTGCTACACATTTGGGAGTTTACAGCCTCCCTGGCTTCTACCCA CTAGATGCCAGCA(G/A)CACAAACCCCTCCCAACAATCATGAAATGAAATGCTCTTAGACAT GCCAATATACCTTTGGGACAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110 GA	---	---	AATGAGTCATTTGGAGTTAGAGGAGTTACTGAAATGGTGACTCCAATGGTGGGATTGGAAGAG GAAGTCGATAATTTAACATATGGTTCTTGCAAGGAATCG(G/A)CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGATATCTAGTGACCCCATGGCTAGAGTTCCTGAC CCTGCTACGGGAAACATTGAATGCA
WI-5403	199 TG	---	---	ACCAACCGTTGGCAAGGCTCCCAAGACTCACCCCACTTTGGTCTTACCTATGCGCGGGTG GGATTGAAGAAATAACATAAATATGTTGCTACAAATTTTCCAGTAGTTACAGGCCACCGCTAT TGGAAGAAATCATAAATGAACCTACAATGATTTGCTCTGGCTTGGTGGCCAGGCATAGAGTTTG JGGCCTACAACCCATTTATCATTTGAACCCCTCAAGAGCATCCAGTTGGGGCT
WI-5801b	157 GA	---	---	TGGTATTTTCTCTTAAATGTTATGATAATTAGTGCTTTGTAGAATTTGAAAAATGTAA TCAGAGAACAGAAAAAATAAGTATAGTTGAAACCTCTACAATTTTAGATTTTAAAGCCCTAG GGAAAGAAAGAGACCTGGGA(G/A)AGGGAATGAGAAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAGGAAGTAAGT

WI-5801a	48	A G	---	---	TGGTATTTTCCTTAAATGTTATGATTATAGTGTCTTTGTAGGAAATTTGAAATAATGT AAATCAGAGAACAGAAAGAAATAAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCTGGGAAGGGAATGAGAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAGTTAAGT
WI-5696	61	C A	---	---	TTCTATTAAATCCTGTGCCCATTTGCAAGACTGCATTCAGTCTGATGAGCCTTAGTTTCATAA AAGCCCTCTCACACCGAGGACAAATGTTCAAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGCAAGAGACAAATCAGGCAGACTGGGAGACC TTATAATAGATTATAAGGCTGTGTGAGTTTATTTAATT
WI-7461	153	C T	---	---	TATTACTAGTTTCATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCACGCTCCTCACTTCCCTTCGAACCCAGCTCAGAGTACACATTTAGGCTGCACATTTCCCTG TGGCAGGGAGTGTCTCTCTGTTCCCTGTTGGTCCCGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTACATGTGTGCA
WI-9716	221	G A	---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTATCTTCTCTTCTGAAGACCAACCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGTACTTCTCTACATTCCTGAAACCTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAAATCTAGAAG/GA/AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C T	---	---	TTTGTGTTAAGTCTTGTGAAGCCACACAGAGTGTACTCTCTTTAC/C/TAAGTGTTCATTTGCA TATATTTATGGGATGATCTATCCTACTTAAGATTTCCTCTCTCAGGTTAAATATTCATTTCTCT TTGTTACGAGGATTTCTTATTTGGCCTTCTTCTAAACCTTAACCATCTGCTTATTTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A C	---	---	GAAACCTCGTTGGCTCAAAGGAACTGTAG/C/JAAATTCCTTTTATTTTATTTTGTGTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCTCTTTTGTGTTGTTAAATCTCTCTAGT GGGCATTTGCAAAAGCAATTTAGACAAAGGTGGTGGCATGGAGTTGTGTGAGGTGCTGAAAG TAGCAATGGAAAGAAAGGTTAATGGA
WI-10312	41	A G	---	---	AAGCCCCAGTGGGAAAGACAGACAAAACACTCCAAAGATAC/JAGAGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGCAATGTCAGACCAAGAACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGTGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAATAAC AGTGACTAAACTGAGGTAGAGTCACAGAGAAATTTCA
WI-11152	179	C T	---	---	GATCTTTGCGACATGCAGACAGATAGCGGCAAGGATCTTGGCATTGGAAGGAAACGAGCCCTA ATTCTATAGAAACAGACTCTACAAAGGACCAGTTAAAGGCTCCGACACAGGGAGCTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCA/C/TCTGTGTGCAAAACATTGAA AACGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	---	TGGTGAGGAGCTGAAGCTGAAGAATAGTCTCTGCTCTGGTCTTCGTTGGAATGGATGAGTCTCT TTTACAAAATTTTCTCTGCTGCCATGGGTGTTATGTTTGAATCATGGAGTGGAGGCTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACITGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGGCCCTTCCTGTAA
WI-4701	198 GA ---	---	---	GGGTTCATTTAACAGCCTTCCACTGGGTCTCAGATTGCAGGAGATGAAAAATAGGAAGAGATAG AAAATGGTGGCCCACTATTGACTTGATACACCTACAAAACACACATTAAACTCTCCCCACTCTTA CCGCCAAAGTCTACCTTTTGGTCTCTTTTATTTCTGCTAATGACCATCTATTTCCCAATTAGAG/GA CCATGTCTATTTTCAGAAAAGCAGTATA
WI-4823	164 CA ---	---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATCTTTACGTAATTTTAAATCATGTCTTTAATTA TGCACCTTACTGTGTGGCTACCAGACATTTCTCAATTTGTTAAATTCCTTAACAACAGCAAGCATAACT GATGTGTCATCTTTTGTATTTCTTAAAC/AJAAAGAAAAGTCTTTTGTGCATCTGCCCTCTCTGT CTCTCTGTTTCACCTCTCTGTTATTTCCCTATTCCAGCATTCATGATTA
WI-4860	72 A G ---	---	---	AAAAAACAACCTTCATTGACATTTCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTT GATTTA/GJGGAGATAAAACCTGTCTCTAAGAAAATTAACCAAAGCAGTACACTAAAATAGCCT TTGTGTGGTTCAGGAAGAAAGCCAACTCCAACTAAGTTGCTAAGAAAAAATATGTTTCATATCA CTCCTAACCTCCACATAGAGCATTATATAGCA
WI-9705	111 CA ---	---	---	TGAAGGAGCAGTTTGAATGCTTACCAGGTAAAGTAAATCGGAGGGGAGGAGTAGGAGTTGCTT CCGGATGTGCAATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCQC/AJAAAATTTTAACACTGATGC TGTCTACAAACGCACATAGAAATCGGTGTAGATTGCGGTTCTCTAGTAGCTAATGTTTAGATA TGATTTGTAATTTGTTGCTGTGTTCTTGGTG
TGR- A004248	177 A G ---	---	---	CAAATACTCTCTGTAGAGTTGCTCTAGGGCCATGGATTCTAAGGGTGGGGCAGGGTGGACTG AAGATCTGTGGCAGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTCTATGAGATCCCAT CTGGCAATACGGTTATCCCGTGGTCTTCTACAGCCACAGAG/GTCCCTCCAATTTAGGGGCTCC GTGGGATGGTGGAGCCAAATGAAGCACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	---	GGGATCAATGTGTGTCTCATCCAAATAGCACT/GJCATGACCTCAGCCCATCTCTTTCTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCTTCTCTAGGGGATCAATAATTTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTCTGGGATCAATTTCTATGGAGCC TGGGGAGAGGGATCTTCTAGTTGA
WI-7747b	88 T G ---	---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTGTTAACTGTGTATGACATA TATATATTTTAAATTTGTTG/JAAAGCTGATTTACTGTCAATAACAGCTTCATGCCCTTGTAAATT ATTTCTGTTTGTGTTGGGTATCTGCCAGTGTGTTTGTAAATAGAGATTGGAGCACTCTGA GTTACCATTGTAAATAAGTATATAATTTTATGTTTGTTCGTA

WI-7747a	44 T C	---	---	---	GTGAGGGAGGCTGACCTACAGATGAACCTCTTCTGGCCTGCTCTTCTGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAAGCTTCAATGCGTTTGTAAAGTTGGAGCACTCTGA ATTCTGTGTTGTTGTTGGGTATCCTGCCAGTGTGTTGTAATAAGAGATTGGAGCACTCTGA GTTACCAATTGTAATAAGATATAATTTTATGTTTGTGTTCTGA
WI-7189	197 T C	---	---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCTCAAAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCAATTTATTTCCCTTCAAAACAAATAATTTTACAGAACGAGGACAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAAGCTTACAAACATTTTTC/JAG TTTGCAATAGAACTAATAC TGGTGAAATTTACCTTAAACCTTGGTTAAT
WI-7850	57 G A	---	---	---	AGCCCCAGCTGGACTCATGGATGTGACCCCTTGTCCCTGCTCTTCTGCTCTGGG/GA/CATGTA TCTGGCAGCTCTGTACCCCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCTGCTGCTGAAGCT GAGAGGCACAGGGCAAGGAGGACAGGACAGAGCCCTCAGCCAGGATCCGCTCTCATTTT ATTGGTATGATGAATGGAAATGAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69 G C	---	---	---	CTCTCTCTCCCATCCATCCACCCCTAAATAGGTAGGTAGGAGGCTGGGAAAGAGGTGGAGGAGG G/GC/JAGAGTGAGGAGATAGGAAGGATTAACCTCTCTGTGTTATTTTAAAGAAACATTTGTT GGTGGCAGCAATCTCCCTGCTCCTATCAGCTGTAGAGGCTAATTTATCTATAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATTATGTCAAAAGTTTAAAT
WI-7919	242 T C	---	---	---	GAAGCAGCTGGATCACTTCCCGAGTCTTGGGAGCGCTTGTGTGGAACACGAGAGCTCTCTCT CAGGGCCTGGCACTCACCTTCTATTCTGTATGATGTTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTAGATTTTCTTACCTAATCTGTTTAAATTTGTAACCTTTATCCATTTGAAAGTGCA AGCCCAATCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACTTT
WI-7928	101 T G	---	---	---	CTCCCTCTCTATGCTCTCAGCAGCAGCTTGGGCGCACACTTGTCTCTGACCGTTTGTGGGCTA TTCCCTTGCACTGCAGACATCGTCAAAATTCAT/GJACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGGCACTTTAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCTCATTAATAAATAACGTACATTTGAGGTAATGGTA
WI-7936	131 T A	---	---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTAATATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAACTTAJ ACTGAATGAAGAAGTATTTGGTAACCGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAGATATATTAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C	---	---	---	TACAGTTCCAGCCGTTGCCCACTCATCTGCGGCTTTGCTTTGGTTGGGGGCGAGATTGGGTTGG AATGCTTTCCATCTCCAGAGACTTTTCATGT/CJAGCCCCAAAGTACAGCCCTGGACCCCTGGTGTG TGTAGTAGTAAGATTACCCCTGAGCTGAGCCTGAGCCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAGAGTGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	TTTCTAGGCTGATACGCTGATGATGATTTTTTTTATAAAATTTCTATACCTCTTGGAATTTGGAATCTTT TTTACTTTGAGCATATATTTTGAATAATGTGTATGTTTAAAGGATCTCCAAATGTCTGCAGATGTG AAGCGAGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGGCTTAAACTGGTCAGTATTAATGTGTAGC CTTACCAAAATAGCCAGTAGTATCTGAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	GGCCAGAGATTAGCAACAAGGATTCATCTGTGTTACTTACTTGGCCCTTTTATCTTCCCTCTGGCC CAGTCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAGACACTCAGTGTCCCTTGGCAGTGC TG/TCTACTCCTCAGGTGACATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACTGAAGAACACTCAAAAATGGCAAAATGTCTATCAG
WI-140	252 C T ---	ATTGTGAAGATTTGGAGGCTTGCAGAGAAATAGATTTCAATTTGGATCCCCAAACTATAATGACA AGTTTTAAATTAGGTGTGATCAAGGCTCTAAAGTGAATTTCAAGTGTGTACAGTAAAGTTTATA TCTTCCATTACGCCAGCTCATTTTGGCAGAAAATTCAGGTGAGTGGATGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTTAAAAATGTGTCAATTTGTCTGTTATGGCATTCCTC/ GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTCTGGCACC CATGATGGAACCTCTGCCATGGTTTAGTACCCCTGGACCAAGTATCCATCCCTGACTTTTAAAA TTCTAAACAGCCCTTGATGGGACAATCTCTGCTAAAGACTAACCCATCTTCTATCTTACGCTA CCTGCTCCCTTTCTC/TGTTTAAACAAGCATAGATAATCTGAACAACT
WI-198	218 C T ---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTGT/CCCAAAGGCTTGATGGGAAAACTCAACATTTGTACCTTAAAGAAAGAGGATGT ATCTACTTTGTTTAAAAAATGCAATATGCTTTATTTTGTAGTTCCC
WI-205c	146 T C ---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTTGT/CCCAAAGGCTTGATGGGAAAACTCAACATTTGTACCTTAAAGAAAGAGGATGT ATCTACTTTGTTTAAAAAATGCAATATGCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCTGGGCCATATGGCTAATAGGAGCTTGAGCA GGGATTCACCTGTTTGAACCCCAAGTCTTCCAAAGGCTCTCAGACTACCTCTCCATCTCCCTCCCT CTCCCCACACACACAATAACAGAGATTGT/CJAATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACAGATTAATCTCTGGTGCTTTAGTTTCTCAATGGGAAATGG
WI-234	155 G C ---	AGCTTTTGAATCCAAAAACCAATATG/TGCTGACTCTTATCCTCTCTTGTGTAACTATCTCC CTGAGGCAAGAAATACAGACACCTGTGGCTGGCTGAAAGGAGGAGGATGGGGCGGAGACAT CGGTGAATGTATCAAAAGCATCTCTGTGCCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGCTTTGTCTTATCCTCTTGTCTATCCCTGATGACTGGGCAAA
WI-276h	25 A G ---	

WI-276	25 A G ---	AGCTTTTGAATCCAAAAACACATAGCTTGACTCTCTTATCTCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCTGTGGCTGCTGACGGAGGAGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTTATCCTCTCTGCTATCCTGATGACTGGGCAAA
WI-427	59 GA ---	TTTTCCCAATCCACAGGTAAACTAATAATGATGTATAGAATTTAGAACTACTTCGAG/AGTTT TTTCCCTGGGGAATAATCACAACCATTTTGGTCTGCAATCAGGTTAAAGACATAGTGTGCA TTTGTATCAGACAGGTAGAGGCTGACTCTGCGAGGATAGCTACCACTAGCTGTGAGACTTTATGT ATTCAITTTATAGAGCCAGGGTCTTGCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	CTCTTCACTCAACACTATATTGCTTACTTAACTGTTACAGATTAGCCACAGAAAGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA/CTAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTTCTCCACTTCC
WI-562b	106 T C ---	CTCTTCACTCCAACTATATTGCTTACTTAACTGTTACAGATTAGCCACAGAAAGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA/CTAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTTCTCCACTTCC
WI-562	103 T C ---	CTCTTCACTCCAACTATATTGCTTACTTAACTGTTACAGATTAGCCACAGAAAGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA/CTAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTTCTCCACTTCC
WI-597c	141 A G ---	GTGTAATTTGGTGGCTTTGCACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATCT GATACATG/AGTAAAGACCTCCATGACTCTGGTACCTCATCATTACCAATGTGAGAAATTAAAC TTGATCTAATATCTTCAACACTAATATACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ---	GTGTAATTTGGTGGCTTTGCACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATCT GATACATG/AGTAAAGACCTCCATGACTCTGGTACCTCATCATTACCAATGTGAGAAATTAAAC TTGATCTAATATCTTCAACACTAATATACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ---	GTGTAATTTGGTGGCTTTGCACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATCT GATGICATGATAAGACCTCCATGACTCTGGTACCTCATCATTACCAATGTGAGAAATTAAAC TTGATCTAATATCTTCAACACTAATATACCTGAGAGAAATAAGTCTATTAAAT

WI-811	66 G C	TTCAAAATTTAACACATTGGGTATATTAATAATTNGCTCTATCCATAGTTCAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTCTTACGTATTACGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCACCCCTACTTGGGCTCTGACTTCCTTCTCTGGGCT GAACCTTCTCTGTGTGCTGTGCGCTTCCCTCTGCTGGCTGCGCTCCATAC
WI-681b	156 A G	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTATAGCTATTAGTTATATCTATGTCACCACTTTGGACACAGATTATATATGTCAGA CACCCAGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCAATGGTTT
WI-681	156 A G	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTATAGCTATTAGTTATATCTATGTCACCACTTTGGACACAGATTATATATGTCAGA CACCCAGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCAATGGTTT
WI-867b	119 G A	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGACATCTTCCCTTTTCATCTCCG/GA/TTTGTGTTTGGC CAAATAATCTCCCGAGGAGTCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCACAAAGCACACATTAGAACTTA
WI-867	113 A G	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGACATCTTCCCTTTTCATCTCCG/GA/TTTGTGTTTGGC CAAATAATCTCCCGAGGAGTCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCACAAAGCACACATTAGAACTTA
WI-867	119 G A	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGACATCTTCCCTTTTCATCTCCG/GA/TTTGTGTTTGGC CAAATAATCTCCCGAGGAGTCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCACAAAGCACACATTAGAACTTA
WI-871b	123 C G	TCATCAGACCTGAGATTACGATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATGAAGACACCCACCTACCTCATG/C/GAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAGTTTGTATGCCTGTTTGGCCTGAATTTGTATGCC TAAATTCATATGTTGAAGCCCTTAACCCCAATATGCTGTTTGTACATAA
WI-871	123 C G	TCATCAGACCTGAGATTACGATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATGAAGACACCCACCTACCTCATG/C/GAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAGTTTGTATGCCTGTTTGGCCTGAATTTGTATGCC TAAATTCATATGTTGAAGCCCTTAACCCCAATATGCTGTTTGTACATAA

WI-884	198	T C ...	AGGTTCTGGACTTGATCTGGGAACAATGGTCTGGGAAATTCCTATTTTGGATTTTCACAGAT CAGTAGAGCCAAATGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTTCTGATCTATTGGGA ACTTCTCTTAATAGATCAGGAAATCCACCTCATTTTAATCATGGACACACNNAAAAGGAATATTCG ATCCGCGATGCAACATTTATTAGTGAAACATGATGAAATGAACATAAT
WI-921b	205	G A ...	CACCTCCAAAGGCTCTGGGGGANGAGCGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTCTGCGAGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGAGAGTATACTGG CAGTGATGCTCTCACGCTGCCCCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCCTGATGGGAGAGATCTGACAAATTTAATCAGGAGGAATTTCTCCGAG
WI-921	205	G A ...	CACCTCCAAAGGCTCTGGGGGANGAGCGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTCTGCGAGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGAGAGTATACTGG CAGTGATGCTCTCACGCTGCCCCCCCCAAGAAAGTCTTNGCCAGGAAAGCAGCATCCATCTAC TCCTGATGGGAGAGATCTGACAAATTTAATCAGGAGGAATTTCTCCGAG
WI-945c	90	G C ...	GGCTGGGATGAGAGGTCTACTTGTGTTACTGGAGGTTTCACTGGCTTGTCTAGAACTAGNAAGNA GAAAGAGACAGNGATTGGCTAACGTCATGCGATGCGAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCAGCANNNGGTT TTCTCTGGTCATAGAACTCTTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90	G C ...	GGCTGGGATGAGAGGTCTACTTGTGTTACTGGAGGTTTCACTGGCTTGTCTAGAACTAGNAAGNA GAAAGAGACAGNGATTGGCTAACGTCATGCGATGCGAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCAGCANNNGGTT TTCTCTGGTCATAGAACTCTTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167	C T ...	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTTATTCATTCAGCAACCTAAATTTGTTTGGATACAT ATCAAGCACAGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ...	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTTATTCATTCAGCAACCTAAATTTGTTTGGATACAT ATCAAGCACAGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ...	TCCCACTGAGTATGGCTTCAGTAGTTTATATGATGCGCTAGGTACATTTGTTTATTGTTCTG CGAATGTTGTTATCTTGGGAGAAATGCTCAACTATAAATATGCTTCTGACCCCTTTCTGTGTT CTTCTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTATTCGCTGTTTACTCTCCTCTG ATTTTTTCCATTATTTTATGCTCTGGCTTCATTTTGTAAATNTG

WI-1147b	204	G A	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTAACTGTATGACTTCTATCCAGCCACCGCAAACTTCTCCTCCTCCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCATTGTTAGGATGAACCTTATCTGGCCAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147	C T	GCATTGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAAATGATGGTCTCCTGAGTGTCTGAAATG/GGCCAGGT TAAGTCTGGGGC/TTCTGGGGTCAGGCTGCTGGGTCACATCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G	GCATTGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAATACAAATGATGGTCTCCTGAGTGTCTGAAATG/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCTGGGTACATCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C	AAGTTTACAGAAAAAATACAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCTGAGACAGCCATTTCTTTTGAATGNT/0JGNCA AAAAATGATTTGAAATTTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202	C T	TTCTCAATTCCTCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTCTCACA TCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA
WI-1305c	46	C T	TTCTCAATTCCTCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTCTCCTC ACATCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA
WI-1305b	153	T C	TTCTCAATTCCTCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTCTCCTCACA TCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA
WI-1305	202	C T	TTCTCAATTCCTCAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTCTCCTCACA TCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA

WI-1306b	248	A G	---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAACTCTGTNGNNNTNG GGCTGGGTGACTGTCCCTGGGTCAITTAGAGCCATAGAGTGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGGCCCTNNITTCGTGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAATTTATCTTCTCTA/GJGC
WI-1306	240	A G	---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAACTCTGTNGNNNTNG GGCTGGGTGACTGTCCCTGGGTCAITTAGAGCCATAGAGTGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGGCCCTNNITTCGTGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAATTTATCTTCTCTA/GJGC
WI-1307b	118	T C	---	---	GACAAGGCTGGTACTAGTTTCCAAATTCCTGATGACCTTCTCTACCTTCTCAAGTGGACA GATTTCTGCATTATACCTGTTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCTCTTAAATGATCTTCTTCTAATATGCTAAACCGGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
WI-1307	118	T C	---	---	GACAAGGCTGGTACTAGTTTCCAAATTCCTGATGACCTTCTCTACCTTCTCAAGTGGACA GATTTCTGCATTATACCTGTTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCTCTTAAATGATCTTCTTCTAATATGCTAAACCGGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
WI-1325b	169	T C	---	---	GAGAGATGGCCCAAGACAAGCAGAGGGAGAGAGCAACCTCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTCCTTTCCTCTC/CJACCTCAGAACCTCTTGAGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T	---	---	GAGAGATGGCCCAAGACAAGCAGAGGGAGAGAGCAACCTCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTCCTTTCCTCTC/CJACCTCAGAACCTCTTGAGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C	---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAGTCTGTTATTGTAAA ACACCAAGTGGGTTTATGGAATGCGTATGTGTGAGTNCATATTACGACAGCTGGGGANGACTC CAGGACACTATGAGCTGAGAGTCTGTCGAGAGTGGTGGTGGTACCCAGGCTCCCCAAATGTAGT TCTTGNCTGAAAGTCTCTCTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175	C G	---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAGTCTGTTATTGTAAA ACACCAAGTGGGTTTATGGAATGCGTATGTGTGAGTNCATATTACGACAGCTGGGGANGACTC CAGGACACTATGAGCTGAGAGTCTGTCGAGAGTGGTGGTGGTACCCAGGCTCCCCAAATGTAGT TCTTGNCTGAAAGTCTCTCTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136 G A	---	---	TATCAGCATGATTGGCTGTGGACACAAGTCAATTTGTACTTTTGTGNNNTCTTTCTTCTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTTNAATTAACCCAGC [G/A]GGATTGTGATGGATCTGTTATTTCTCTGTCTTGGAAACAGAGAGTCTCTCTGNGAGNTG GTTTCAGGAATTTGCTCTGTTCCAGAGCCACTTGCACITAGCAAGTGT
WI-1349e	192 G C	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTGAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349d	264 C A	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTGAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349c	192 G C	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTGAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349b	264 C A	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTGAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349	264 C A	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTGAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1403b	57 C T	---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTACATCAACATAATTTCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C	---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT TAAAGTTTACATCAACATAATTTCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T	CAGCCGGAAGAGATACGTGGAGAGATGTC/TTTGGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGSCATTTGGAGGGCCCGCAGAAAGATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGAGGTTTAAAGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGGCGGTTGC AGCGAGGCCCTTAGGTCGGTATTTAATGTTTGTAGAAAAAGTCGC
WI-1417b	31 C T	CAGCCGGAAGAGATCAGTGGAGAGATGTC/TTTGGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGSCATTTGGAGGGCCCGCAGAAAGATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGAGGTTTAAAGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGGCGGTTGC AGCGAGGCCCTTAGGTCGGTATTTAATGTTTGTAGAAAAAGTCGC
WI-1729	172 A	CCATGAGCAACAGCATGTTCTACTCTGTGATGTATGTAGGGGCGCATGTATCTGTATTCTT TTTTATCTCTCCAAAAGAAATTTTCAATATGCAAAACATTTACAGGCAATGCAGCTCGTAATAAGA TGTTGAGAACTGAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACATTTCCAGCA GATGTATGTGCTTCCTCGTGTGTTACCTTCTCTCCACCATCACTGCTGTTTTT
WI-1732b	122 T C	TGCCTTACTTCTTTGTTCATTCCACCATTACATTTTGTAAATGGAACTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGAGGAGTNTCCCTGGGTCAACCCCTTTTCAITCAGTCT CTGCCACATGCTAGTAAGTGTGAGTGGTGGTGCATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTACTTATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T	TGCCTTACTTCTTTGTTCATTCCACCATTACATTTTGTAAATGGAACTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGAGGAGTNTCCCTGGGTCAACCCCTTTTCAITCAGTCT CTGCCACATGCTAGTAAGTGTGAGTGGTGGTGCATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTTCACACTACTTATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G	GGCAATTAATGACTCCAAAGGTAGTAATCCCTTCCCAAAAAGGTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACTTGGTGG/TTTAAAGGTGTCTGTTTCTGGCAAGAGTCAG TGGAGGTGTCCGGGAAAAGGGCTAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTGCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G	GGTACACAAAAGAAATGCTCTGGAATCTACAGGTAGCCCTTAACTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACATGAAGCTGGGCAAGAAACAAATCTCTAGGAAAGTACAAATTAC TGGAACTGTAGAACAAATATCTCATAGTTTACACATAGCTGGGAATCACTATGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAAATATCATAAAAAT
WI-1803c	77 A G	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTAGGACACATAATATTTTTCAGGCAGAA CCATTATGATGAGTATGAGTGGTAGCATACACACTTGGGAGGACATATTTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGCAAAATTAATTAATCTGTTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G	...	CCACTCAGTAATAGTGTGGAGTAAGTATGGTAGGCACATAATAATATTTCCAGGCAGAA CCATTATGATAGTAGGAGGATAGCATCACACTTGGGAGGACATATCTGGAGTAGATATCCTG GGTCTAATTTCAATATATCTACTAAGCATGACTTCTAGAAAATTTACTTATTACTCTTGTCCCTCAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAATAACTGGAAATCA
WI-1837b	112 C T	...	TTACTTGGGATTTTTCATAGCTGATCAATTTACCAITTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAACCCGTTTATACIC/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTCACCTGATGCCAAACAAACCTCAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACTTTAGCTTCTGCTGGCT
WI-1837	112 C T	...	TTACTTGGGATTTTTCATAGCTGATCAATTTACCAITTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAACCCGTTTATACIC/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTCACCTGATGCCAAACAAACCTCAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACTTTAGCTTCTGCTGGCT
WI-1840b	79 G T	...	TCACCTAGGGAGGTCGCTAAAAATGAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TGAGAACTCTGAATATTCAGCACATACAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T	...	TCACCTAGGGAGGTCGCTAAAAATGAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TGAGAACTCTGAATATTCAGCACATACAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T	...	GGGCTCACTTTCATCAGAGCACATATCAGTGATGCTGTTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTGAGGTAAAGGACCTGCNNTTTTAC/TGTC/GCNAAATAAACTCCAAAA AAGTGTAGTCCACAGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T	...	GGGCTCACTTTCATCAGAGCACATATCAGTGATGCTGTTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTGAGGTAAAGGACCTGCNNTTTTAC/TGTC/GCNAAATAAACTCCAAAA AAGTGTAGTCCACAGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T	...	TGTTCTCTGGTCCAGGACCGGCTAAGTCTGTGTCATATGAATAATCAACTGACAAACCCGNG CTNAGGTAGGNTACCTNGGCAATAGCCCATCTTACAGCTGCAAAAGAGGCTTCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACACTAGAGAGAGCGCAACAGGTTTGAACCCAGCTCTGCTGCT GACTTCAGATCTGTGCTTAAGTGGCATGAGAAACCACTTTTCTTGTCTCC

WI-2013	127 C T	---	---	CTTTAGAGGTGGTCATTCGGTCCCTCTCGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACGACACTGCTCTCA CCAGAAAAAGAGAAATACCATCATGAGGAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCAGCTTCTGAGCCCTGGTACTGCAATCC
WI-2032c	166 G A	---	---	ACCAGACATCCATCAGGAGTTAGTCTCTGCGAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAAATTTTCTTACTTACTATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTTAACC ACATCACCCTGCTTCTAGATGTACAGTGTGGGACCTCTGCTCAACCTCCGACTTTCACAGA AGATCATGGTTAGGCTCACCTCTCTGTAATTCCTGTTTTCAAAGGG
WI-2032b	219 C G	---	---	ACCAGACATCCATCAGGAGTTAGTCTCTGCGAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAAATTTTCTTACTTACTATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTTAACC ACATCACCCTGCTTCTAGATGTACAGTGTGGGACCTCTGCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCACTGCTCTGTAATTCCTGTTTTCAAAGGG
WI-2032	219 C G	---	---	ACCAGACATCCATCAGGAGTTAGTCTCTGCGAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAAATTTTCTTACTTACTATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTTAACC ACATCACCCTGCTTCTAGATGTACAGTGTGGGACCTCTGCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCACTGCTCTGTAATTCCTGTTTTCAAAGGG
WI-2054b	188 C T	---	---	CGTTTTCTTACATCTTGGGACATAAAGANGAAGAGNAGCTGCTCTTCTGTTGTTGTTGCT CAGAGCTGCTTAGAGCNAGGACAGAGAGGAGGCTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCAGCCAGGCTCAACAGAACTAATACCTGCTGTTCTGCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTACTGGATGGCTGCTCTT
WI-2054	183 T C	---	---	CGTTTTCTTACATCTTGGGACATAAAGANGAAGAGNAGCTGCTCTTCTGTTGTTGTTGCT CAGAGCTGCTTAGAGCNAGGACAGAGAGGAGGCTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCAGCCAGGCTCAACAGAACTAATACCTGCTGTTCTGCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTACTGGATGGCTGCTCTT
WI-2573d	129 T C	---	---	TGGGATTAACCCCTGTTTCTCTCCAGTTCAGTGGCTTAATGTTTGTGCTAGAAATTAACA TTAAGCAGAGTAAATAGCTCTTAAATGACCTTGCCTGTTCAAGGTTTCCGCTGCTTTCCTGGA TATCATCTGATCTCCCAACAGGGCTTATATGCTAGGTAAGGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTGCAAGGCTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C	---	---	TGGGATTAACCCCTGTTTCTCTCCAGTTCAGTGGCTTAATGTTTGTGCTAGAAATTAACA TTAAGCAGAGTAAATAGCTCTTAAATGACCTTGCCTGTTCAAGGTTTCCGCTGCTTTCCTGGA TATCATCTGATCTCCCAACAGGGCTTATATGCTAGGTAAGGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTGCAAGGCTATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---	---	<p>... ---</p> <p>TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCAC TTGCCGTTACAAGGTGTTCCGTGCTTTTCJTGGA TATCATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG</p> <p>TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCAC TTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT TATCATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG CATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG</p>
WI-2573c	165 A C ---	---	<p>... ---</p> <p>TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCAC TTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT TATCATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG CATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG</p>
WI-2573b	165 A C ---	---	<p>... ---</p> <p>TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCAC TTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT TATCATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG CATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG</p>
WI-2573a	129 T C ---	---	<p>... ---</p> <p>TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTTTAAATGCAC TTGCCGTTACAAGGTGTTCCGTGCTTTTGATAT TATCATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG CATCTGATCTCCCAACAGGGCTTATTAATGCTAGGTAGGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCAACAGGTCATATGGCTGGGCTTGGACGAG</p>
WI-2868b	60 A G ---	---	<p>... ---</p> <p>GACTTCATGCTCATGAACAAGCATTTGCTTTAATTTACAGACATTAAGAACAGCTTTCGJAGJCTC CCACTTCCTCCCTCCACTATCACTCAACCTTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAAGTTCTGCTATACAGATTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAATAATGAATATCGATATAC</p> <p>GACTTCATGCTCATGAACAAGCATTTGCTTTAATTTACAGACATTAAGAACAGCTTTCGJAGJCTC CCACTTCCTCCCTCCACTATCACTCAACCTTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAAGTTCTGCTATACAGATTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAATAATGAATATCGATATAC</p>
WI-2868	60 A G ---	---	<p>... ---</p> <p>CATGCTGTGAACCTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATGTATATCTCTAGGC TTCAAGGAGCTTCTCATCTCATTTAGGAGAGCAAGATGAACATCAGGAAATGACTGGATAATGATGATC AGAAATGAATAGAGCCCACTTTTAAATTTATACAGCTTATGTCACACTTCTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT</p>
WI-2870b	131 T C ---	---	<p>... ---</p> <p>CATGCTGTGAACCTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATGTATATCTCTAGGC TTCAAGGAGCTTCTCATCTCATTTAGGAGAGCAAGATGAACATCAGGAAATGACTGGATAATGATGATC AGAAATGAATAGAGCCCACTTTTAAATTTATACAGCTTATGTCACACTTCTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT</p>
WI-2870	131 T C ---	---	<p>... ---</p> <p>CATGCTGTGAACCTCTGTGCTGCTTGTGCTGGGGAATTAGAGCAAGGAATGTATATCTCTAGGC TTCAAGGAGCTTCTCATCTCATTTAGGAGAGCAAGATGAACATCAGGAAATGACTGGATAATGATGATC AGAAATGAATAGAGCCCACTTTTAAATTTATACAGCTTATGTCACACTTCTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT</p>

WI-2954c	49	T A	TTAGCACATATCTGTGTGGGACTTAACGTAGACAAAGGCAGTAAATAATACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTACCTACCCCTCCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41	A G	TTAGCACATATCTGTGTGGGACTTAACGTAGACAAAGGCAGTAAATAATACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTACCTACCCCTCCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38	G T	TTAGCACATATCTGTGTGGGACTTAACGTAGACAAAGGCAGTAAATAATACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTACCTACCCCTCCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62	T C	ATTACAAATCTACCTAGCACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGATC/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAAACCTCCTCCTTCCCTTAATAAACCTAAG ATTTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTCTAGATGTATGTCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2971	62	T C	ATTACAAATCTACCTAGCACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGATC/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAAACCTCCTCCTTCCCTTAATAAACCTAAG ATTTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTCTAGATGTATGTCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133	A T	TTCTGGGAAAGAAAGATGGGGTTTTTNTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCGGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	G C	TTCTGGGAAAGAAAGATGGGGTTTTTNTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCGGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	A T	TTCTGGGAAAGAAAGATGGGGTTTTTNTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCGGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 GC	---	---	TTCTCTGGGAAAGAAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCGAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAGG AATGAGACAGAAGCTAGCAGAAAAGTGTT
WI-2995d	133 AT	---	---	TTCTCTGGGAAAGAAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCGAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAGG AATGAGACAGAAGCTAGCAGAAAAGTGTT
WI-2995c	151 GC	---	---	TTCTCTGGGAAAGAAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCGAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAGG AATGAGACAGAAGCTAGCAGAAAAGTGTT
WI-2995b	151 GC	---	---	TTCTCTGGGAAAGAAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCGAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAGG AATGAGACAGAAGCTAGCAGAAAAGTGTT
WI-2995a	133 AT	---	---	TTCTCTGGGAAAGAAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCGAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAGG AATGAGACAGAAGCTAGCAGAAAAGTGTT
WI-3147	85 CT	---	---	ATCTGTAATGTTTTCTACTGCTCCAGTAAATTTCTTATGAGGTCATGTCACCTCTACTTAT T/CJGACAAGCAAGAACACACAGAAAAGCCCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATACATCTTATATCAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAAATGACTATTATTINATCTCTAT ATTTCTGTAATGTTTTCTACTGCTTCCAGTAAATCTTTTATGAGGTCATGTCACCTCTACTTAT T/CJGACAAGCAAGAACACACAGAAAAGCCCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATACATCTTATATCAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAAATGACTATTATTINATCTCTAT
WI-3234b	68 TC	---	---	ATTTCTGTAATGTTTTCTACTGCTTCCAGTAAATCTTTTATGAGGTCATGTCACCTCTACTTAT T/CJGACAAGCAAGAACACACAGAAAAGCCCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATACATCTTATATCAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAAATGACTATTATTINATCTCTAT
WI-3234	68 TC	---	---	ATTTCTGTAATGTTTTCTACTGCTTCCAGTAAATCTTTTATGAGGTCATGTCACCTCTACTTAT T/CJGACAAGCAAGAACACACAGAAAAGCCCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATACATCTTATATCAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAAATGACTATTATTINATCTCTAT

WI-3292b	106	GA	---			<p>GTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCGCACTATCC TCCCTGTCCTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGATTGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGATTAATTAATTAAGTAAATATATTATTTNCCATGA GACACAATGGAAATGGAAACATTCATGGAAAAAACCCATTTCATC</p>
WI-3292	106	GA	---			<p>GTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCGCACTATCC TCCCTGTCCTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGATTGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGATTAATTAATTAAGTAAATATATTATTTNCCATGA GACACAATGGAAATGGAAACATTCATGGAAAAAACCCATTTCATC</p>
WI-3355	19	GC	---			<p>CCATGAACCATGGCTACA/GC/ATATTCCTAACTTCAGAGTCCCTTACTGGAGGGATCCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATCTATTCCTCCAGCACTTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATCTTTTGGATCAGTTTAGATGACTTTNAGTTG</p>
WI-3408	194	GA	---			<p>CCATGAAGAAATGAGTTCCCTCCCTGGGTACGCTAAGAATAGCACACCTTGAGAAATTTNACT TAGCAGTGGCATTTGTAATGGCTGGATTTCCTCCGCTTAAGACACACACCTTATGCTTTTCAAGCTTT CTGGAAATGGGATGAATC/TNACATTCATGTCACCCCTCGTGGGATCAGTCTCTCQ/GA/JGCCCC ATCTCTGNAGAACCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG</p>
WI-3505b	131	GA	---			<p>TAACCTATGCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACCTTAAAAATATTTT GAAAAATGGCAATTTTAAATATCTTTTGGAACTTCCTAACACATTAACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT</p>
WI-3505	131	GA	---			<p>TAACCTATGCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACCTTAAAAATATTTT GAAAAATGGCAATTTTAAATATCTTTTGGAACTTCCTAACACATTAACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT</p>
WI-3564b	177	CT	---			<p>GCTAGTAGGTTCCACCTAAATGGTTCCAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGCTCTCCAGAGTATTCACATGGCAGAGTGCACAGAGGCTTGAGCGTCTGAGCG TGGGACTTCACTGTTGACTACGTTAACATGCATGCTGTTCTTACAAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTCTCACAAAAACAAA</p>
WI-3564	177	CT	---			<p>GCTAGTAGGTTCCACCTAAATGGTTCCAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGCTCTCCAGAGTATTCACATGGCAGAGTGCACAGAGGCTTGAGCGTCTGAGCG TGGGACTTCACTGTTGACTACGTTAACATGCATGCTGTTCTTACAAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTCTCACAAAAACAAA</p>

[illegible]

WI-4230	93 T	---	---	AGAGACGTTGAATGGGACATCTTTTCTATTTCGATTGTTTAAAGATTGATGAAAA GTTTGTACATCCAGATTATCTTTATAGCAGCAGAACTCTGGCAATAATAACACACACTGACT TTTCCATGGTAAAGAGAGATTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C	---	---	GAAATCCATTGAAGTTTGACCTTGAACCTGATCTCATTAATCTTTTCTAGTGGTTGATTT CATTTTGGACAACAGACAGACGAAAAATTTCCACTTAAATTAATCTCTCTAAGTATCTATGAT TTAGCACTGTAGCACCAAGAACTGTGAAATTACTCTAGATATCTTCAGAACTTAGGATGGAAG AA
WI-4271b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGATNCTACAGGAGCCCCAACCCCTTGTGTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGATNCTACAGGAGCCCCAACCCCTTGTGTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G	---	---	AATCGAAACATTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAGAGAGAAATGAAGGATATTATGCTAAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/ATNGCAAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGAAGCGGTAA
WI-4389	156 G	---	---	AATCGAAACATTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAGAGAGAAATGAAGGATATTATGCTAAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/ATNGCAAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGAAGCGGTAA
WI-4488	31 A	---	---	GATGACAATTATGTGATTGGCATTTTAA/G/GTACCATTCCATTTCTCTGGCTTTCTGGTT TGTTGTTGAGAAAGTCAGGGGTTAGTGTGTTCTCTCTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAAATCAAAATTG TATTATCTATGCTTAAATGCTCAG
WI-4491	145 G	---	---	ACCATCAATGATACCTCTTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAAACCT GTCTTGGACATTGAAAAATAAACATTACTATTGGTCAATTTCTGCTACTTACAAAGTACTGCACCT AACAAAGTTAAG/GC/GTGTTTTGGAGGGGAAATCATAAAAATGCATAAAAAATTTCTACCACCTGCA TTTCTGTGCCATAATAAAATTTTACATGCT

WI-4584	144 A G	TTGGTTGGCATTATAGCCTGATAACAACATATTACAATCATATTGTTACTCTTATTTTACAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGACAGCCAGATTTGAACCCAGGAATCCATT CACCGGTAC/AGTGTCTACCTGGTAAATAATGTTAAATTAATCTATGGCAATTAGATTTCAAAGA GTCTAATGTGGTTTGAATAAGGTGGCTTTAATTTTATCAGTATGC
WI-4639	185 C T	TTCTGCAATTTGAATGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTTTCAGTACAATA TGGTGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTTCAATTTCCACCAATTTAC TGACCATAGACTTGGGGAACAATATCTCACCTATCTGAGTCTGTATCCGTCTCATCTTTAAATTTGTA AATTTTAAGGACACCTATCATAGTAATATTGTGAGGATAAATAAGAAATAA
WI-5327	63 A	AAATGAATCCGCTTTAGACAAATACCAAGTAAGGCTGGTGCAGGATGGTGGCTGAGAGAG/4/- JGATTACTCATAAAAGCATATTAAATTTTATAAATATGGAATAATTAACATAGATAAATTAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAAATGATGAATGTTCTAAGCAGACAG
WI-5390	87 C T	GCCTTTGAGAAATGAAAGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTTTGTGTAT TTATTGTTCACTTATTATTC/TCGTCTCTCCCTCTGGTATGCTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCCGAATTCGGCTCTAGAGGTGCCAGAAAAGTTTCGGTGAATAGAAATG ACGAATGGGTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTAATTAAGCAGT GCAACATTTATTTAATTTT/AAATTTT/AAAGAAACCTGTTTCTGAAACCTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGTGAATCCACCCCATCTCTTTTCCACAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5404	87 G A	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTAATTAAGCAGT GCAACATTTATTTAATTTT/AAATTTT/AAAGAAACCTGTTTCTGAAACCTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGTGAATCCACCCCATCTCTTTTCCACAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5545b	77 A C	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCTC/AC/CCCAACACCTCTGTTTCTGACAGCAAGTTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA
WI-5545	77 A C	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCTC/AC/CCCAACACCTCTGTTTCTGACAGCAAGTTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA

WI-5860b	134	A G	ACTCAAGTTGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTCTAAGATTTTATTTGT TTCCTTTTATATAAATTATGGATTTGTTTACCTTCCCTAACCAACCTTCTAAGGAACTACAC GTTTACTGGAATCATGTGAAGACATTCCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGATCA ATTCCTCAATCATCAACTCTGTAT
WI-5860	134	A G	ACTCAAGTTGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTCTAAGATTTTATTTGT TTCCTTTTATATAAATTATGGATTTGTTTACCTTCCCTAACCAACCTTCTAAGGAACTACAC GTTTACTGGAATCATGTGAAGACATTCCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGATCA ATTCCTCAATCATCAACTCTGTAT
WI-6106	208	C G	GCAACCACTATTACTGATTCCAAACCCAGGTCTACTAACCATTAATCAACCTAACCCACAATAC TATATATGTCCTGTTCTGAAATTTTTCATTTAGAACTCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTCTCCAGGAGTCTCAATGTGAAGTAAATCTTACAGAG TAAATTCGATAGTAGGTCAACCAAGTCTATTTGTATGAAGGAAAG
WI-6109d	129	T C	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGAGGACTATAAGGAGATCAGGTGGAATAAACCGAAGGAAACCTAA AACCCCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAATTTTGATGT GNAATAATTATCCCTGAAATTTTATACCA
WI-6109c	147	T C	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGAGGACTATAAGGAGATCAGGTGGAATAAACCGAAGGAAACCTAA ACCCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAATTTTGATGT TGNAATAATTATCCCTGAAATTTTATACCA
WI-6109b	147	T C	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGAGGACTATAAGGAGATCAGGTGGAATAAACCGAAGGAAACCTAA AACCCCTATATTNCTGTCCTGTCATACCTTTAAATGTATAATGTGGGAGAGAAATTTTGATGT GNAATAATTATCCCTGAAATTTTATACCA
WI-6109a	129	T C	AATGCTATCATCCTTCCATGTCGATACCTGATTTGATTCATATGCTTATTTAGCACCTGTC TTCACACACATGCTTTTGTTCATGATTCGATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C	

WI-6463	72 T C	...	GCTGGAGAGAAAGACCTCCAAAGAGAAAGAACTAAATCAGAGTCTTTGAGCAAGAGAAATTGAAA AGAACATTC/TGAAAAAAATTAAGTAGAACCTCAAGAGCCAAAGTCCCAATTGTGTCATT TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATGATCAGTTAAATGTTCTCTCTCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T	...	AAGCAGTAAATCTTCATCATGCGATGCGATGCGGTAATGTTATAGAACTTCAGAGGANAC AGAGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACITGCTTAGAGCC AAGAAAAAGTAGGATTTGAAGGGCACAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T	...	AAGCAGTAAATCTTCATCATGCGATGCGATGCGGTAATGTTATAGAACTTCAGAGGANAC AGAGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACITGCTTAGAGCC AAGAAAAAGTAGGATTTGAAGGGCACAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A	...	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTACCTCTCCCAATAGTGGAGAAATCAGAGT/A/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A	...	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTACCTCTCCCAATAGTGGAGAAATCAGAGT/A/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A	...	CACATTTGAATGCACTGAGAAANTGGTTTNTAGGCTTACCTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA/GA/ITCAAAATTTTAAAGAGAACAGGAAATAAGGAAGGCCCTAACACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTCTTC
WI-6564b	54 G A	...	TTCCTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTCTCTATGCG/ACACTGGCTTG TAGGCATTACATCATATGCTGTCTGCTGAAAATCTCAATTAATTCCTCNCCTATTCCTTTTCCAT GCTCGCTCATTTNCTCAGAAATGAAGGCAATTTGATTATNATTTTGTGGTCTGTGTAAAG GTCTCTGGCAGGAGAACATGACATATGACTTTAAATAAAGACCAACA
WI-6564	54 G A	...	TTCCTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTCTCTATGCG/ACACTGGCTTG TAGGCATTACATCATATGCTGTCTGCTGAAAATCTCAATTAATTCCTCNCCTATTCCTTTTCCAT GCTCGCTCATTTNCTCAGAAATGAAGGCAATTTGATTATNATTTTGTGGTCTGTGTAAAG GTCTCTGGCAGGAGAACATGACATATGACTTTAAATAAAGACCAACA

[illegible]

WI-6710	106 G A	---	---	CCATGACAGTTTAAITAGGAAGCTTCGACTTGTAGAAATACAGAGGAAGTCCAGTTATCTACCT ATTCTTAAACACATTTTGTGAGGCTGGAATGATTCGCGATAGTAAACACTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTATTAGTGAGTCGACAGGATGTCACCAAGTGAGCCTC ATCCAGTCCCAATGGAGGAGTTGACTTAGACCTTCCTTGACAGGAAGGTC
WI-6766b	148 G C	---	---	AAACAAATGGTGCATTGCATAATTTTGGTCACAGTATAAAACAATACAAATAGTTCATATAAC ATTGGATATGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCCTTAGT GCCACACTTAAAN(GC)AAAGTCAAGTTTCTCTCTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGGNGAAGTTACCCAAATCCAGTTCCCTCTTC
WI-6766	148 G C	---	---	AAACAAATGGTGCATTGCATAATTTTGGTCACAGTATAAAACAATACAAATAGTTCATATAAC ATTGGATATGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCCTTAGT GCCACACTTAAAN(GC)AAAGTCAAGTTTCTCTCTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGGNGAAGTTACCCAAATCCAGTTCCCTCTTC
WI-6787b	97 A G	---	---	ACAGATAAAGTCTTTATCCCTGTATTTTATTAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA ATACTTGTGACAGCAATGTTCAAAATTTCAAGTTTCTACGATAAGATATCTTCATGTACAACGTG ATGCTTGTCTCTTGGGAAGGACGCTTAAAGACCTATGATAACACACATCCACATGACAAAGGA GAGTGAATAGGGCAGAGTAGANTACTACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G	---	---	GAACCCACAGGCTCTGTTATTTTATTAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGCGGCTCTCAAAATCAATCAGTCAACCCGCGAGTTAGAAAGTAGAGTCAATGAGGAA GAGCTGTGCTGTAGGAAGTAGGTTAATGCCCTTAATCCCGGAAAGGGGCGAGACTGAAGCCA GAGCCAGANTCTGGCAATTCACCAAGTTTCTCATCAGGTAAAGGCAAC
WI-6810b	37 T C	---	---	CACAATAATAAATCACTCCCTACCTTGAACATTTAT/CJAGAAAGCATTTTTTAAITTTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTTAAAAATGTCTATGNACAGTACAAATTTCTTTTGTGTTCTGCAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGCGCAATGAAGTTAAT
WI-6810	37 T C	---	---	CACAATAATAAATCACTCCCTACCTTGAACATTTAT/CJAGAAAGCATTTTTTAAITTTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTTAAAAATGTCTATGNACAGTACAAATTTCTTTTGTGTTCTGCAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGCGCAATGAAGTTAAT
WI-6817b	145 C A	---	---	GCATGATTAAACGAGTGCGAAAAATACCAAGTACATTGGGTGAACGATGAGTGTCTTAGTA TTTGGCTTTTGTATCCAGTTAAGACCACATCAGCATATACAACTATCATCACTAACAATGTAGCT GCAGGGTAAACGATGTGGATACCTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAAATCTTGTTCAGGTGCGGCTGTGTGCAG

[illegible]

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WI-7136	58 T C	---	TGTGAAGCCACATTTTCCACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAACGTGTCTCAATTC TCTCAATAACTCAGTGTAGCACTTTAAAGCTGAAGGACAGCAATGAAAGAGCATATCAATGTGTG GTGGAGAAAGGGAAGGGTTGGCTTTTAAATTTATTTCTCATCTTTTAAACAAGAAAGNNNNIN NNNGTAGCTTCTATATATG
WI-7146c	210 A G	---	GGGACGCCGTGTGTTTGGCTCAATTTGGTGTGGTTCACATGGAGCTCTCCATTCCTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTCTCCTTGTGGCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGATGTGTGGCCCTCTCTCCGATGCC AACGC/G/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 A G	---	GGGACGCCGTGTGTTTGGCTCAATTTGGTGTGGTTCACATGGAGCTCTCCATTCCTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTCTCCTTGTGGCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGATGTGTGGCCCTCTCTCCGATGCC AACGC/G/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 GA	---	GGGACGCCGTGTGTTTGGCTCAATTTGGTGTGGTTCACATGGAGCTCTCCATTCCTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTCTCCTTGTGGCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGATGTGTGGCCCTCTCTCCGATGCC TCAACGCCAGTTATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 A T	---	ATATTACAACCTGCTTTTAGTCAATCTTCCATCTCAATGACTCTTTTCTTTATATGTTAAACATA TATAAATGGCACTGATAGTCAATTTGATTTTATCAGGAAGTATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAACNNNNNNNIA/TJAAAAAAGTTATTTAACAGTAATCTATTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156 T G	---	TAGAATAGATGGGTCTATCTCTTGGCTCTGGTTCTCCAGCCCTCATGTTGGCATTACACAT GCCTGATGCCATTAACACAGCTGGCCCTACCCCTTAAATGATCTGCTGCTGCTAAATTAATACAC CAGTGGTTCCTCCTCCTGTGTJAAAGACATATGCTCAGATGCTGTTACGGATATTTATTTCTAG TCTCACTCTGTGTCCACCTCTCTCTCTCCCATCCCACTCCAG
WI-7169b	161 A G	---	AGCTCCACAGATGCAAGTTGGTTTGTGTTTCTGTTATCACTGTCCACAGCTATTAACATGTAT GCTTTTCAGATACAGTTGTCTAGCCAAAGCCATCAAGTCTGTGAATATCAATATGGTTATGCAAT ACAGCAACTTTTATTTAAGTAGATJAG/GGGAGAATATGTTTAAAAATATAGGAATCTCTAGACCATA TTTTCAAGTCACTTACGAGCTAGGATTTCAAAATGGAAGTGTATATATA
WI-7175b	194 C T	---	CTCTAGACTAGTCTTTACCTTTATTAATGAACCTGTGACAGGAAGCCCAAGGACAGTGTCTCTCA ATAACTTACAGGAAGTCAAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAAATCACTATACCATC AGTTACTGGTTTCAGTTGACAAAATATATATGTTTACTGCTGTCAATGTCCATGCCATC/TJAGAT AATTTATTTGTTTGAATAAAAAACAATTTGTACATTCCTGTACTCGG

WI-7175	194 C T	CTCTAGACTAGTCTTTACCTTTATTATGAAGTGTGACAGGAGCCCAAGGCGAGTGTCTCTACCA ATACTTCAGAGAAGTTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCTACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGATGTGCCATGCTTACCTAGAT AATTTATTTTGTATTTTGAATAAACAATTGTACATCTCTGATCTGGG
WI-7178b	273 G A	TGTATCAGGTGAGGACTTGGACAGGAGTCACTGTCTGGCTTTTCTCTGAGCCGAGTGGCTGGAG AGGGTCTGCTGTCACTGGCTGCTTGGGGAACAGACCGTGCACCCAGAAAGCATACACCA ATCCAGGGCTGGCTCTGCACACTAAGAGAAATTTGCACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A	TGTATCAGGTGAGGACTTGGACAGGAGTCACTGTCTGGCTTTTCTCTGAGCCGAGTGGCTGGAG AGGGTCTGCTGTCACTGGCTGCTTGGGGAACAGACCGTGCACCCAGAAAGCATACACCA ATCCAGGGCTGGCTCTGCACACTAAGAGAAATTTGCACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C	GCATATTTGGCAGCTTATGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCAC/ATCTGAGCCCTATCTCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGCTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGTAGCAAGAAATGGCAGCTATTTCTGAAAGCCTAGTACCCCAAT
WI-7182	106 C A	GCATATTTGGCAGCTTATGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCAC/ATCTGAGCCCTATCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGCTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGTAGCAAGAAATGGCAGCTATTTCTGAAAGCCTAGTACCCCAAT
WI-7191b	273 T A	ATAATTGCTTTTCTAGGCTGGAGATATTTTCAAAAGAGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACACACATCTAAGCATTTAGTGATGGTAGC TGATGTGAGCTTCAGTGTGGATTTTAAAGCACTCTAGAAACAATGAAGCTTCTTGGCATATTTAAGGAG CTCCCAAAATGTTTACCTATTAAATTTGAACCTAGCAAGTAGAAGACCAAT
WI-7199c	112 T C	CCAGTGGTGAACAGAACTCCCAATTTGAGTTGCACCCCTCCCTGTGGCTTATGAGCTCAGCCTC GCTTTGAGGTACCAACCGCTCTGTCAGCTCTTGCAGCTTGTGGGCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTTCTTTATAT AGTCTATAGTTTACTCTCAGTTCTCACCATCATCATCTTGTCTAA
WI-7199b	112 T C	CCAGTGGTGAACAGAACTCCCAATTTGAGTTGCACCCCTCCCTGTGGCTTATGAGCTCAGCCTC GCTTTGAGGTACCAACCGCTCTGTCAGCTCTTGCAGCTTGTGGGCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTTCTTTATAT AGTCTATAGTTTACTCTCAGTTCTCACCATCATCATCTTGTCTAA

WI-7216c	237 T C	---	---	TGACACTAACACTCTAAATCAAGCGAATGTTGGAACACCATGACCTCCTGTGTGTGCTCTTCTCCCG AAGGACAAAATGTAGAAAAGATGTGAGATAACTTACTCAAGATCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTGTGAGGCTAAACACAGTTTGTTTTCCTGTGTATACACTT
WI-7216b	237 T C	---	---	TGACACTAACACTCTAAATCAAGCGAATGTTGGAACACCATGACCTCCTGTGTGTGCTCTTCTCCCG AAGGACAAAATGTAGAAAAGATGTGAGATAACTTACTCAAGATCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTGTGAGGCTAAACACAGTTTGTTTTCCTGTGTATACACTT
WI-7220b	147 A T	---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATACCATATTTGTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAATAGCAATCATATGGATAAAGTAGACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGACACACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140 A T	---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATACCATATTTGTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAATAGCAATCATATGGATAAAGTAGACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGACACACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232 C	---	---	GATCGAATTTTCAGATGATCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATA TACATATCACTCCTCTATTTCTTAAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTATCATTT CCCTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTGAATAATA TTACCCCAAAATGCCACCACTTAACGATCTTCACCTCTTGGGGTTT
WI-7228b	254 G A	---	---	ATAGCTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACAGTAATTTGGCTCCCAATTCATAA TATGTTCCACAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAACTTATTTAGTTGATTTTAAITTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAAATCCACA CATATTGTTTAAATAAGAAATGTTATCCAACTATTAAGATATCTCAATGTT
WI-7228a	163 G A	---	---	ATAGCTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACAGTAATTTGGCTCCCAATTCATAA TATGTTCCACAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAACTTATTTAGTTGATTTTAAITTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAAATCC ACACATATGTTTAAATAAGAAATGTTATCCAACTATTAAGATATCTCAATGTT
WI-7233c	213 C T	---	---	CGATCGTACTGCCAGTAGCATGTCTGTCTGCCGGTCTGTTGTACATTCATTTCAATTTGTTACA GATGTGAACCTTATCTCTGTCACTAAATATATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTTACTTCTCTTGTGCACTTTTGTGGCAATTTAAGTGAAGTCTGCTAATA GTGTAAAGTATCTGTGTGCACAAAACCCACTGCCAGATAACCAAGGGGGCCTG

WI-7233b	213 C T	...	CGATCGTACTGCCAGTAGCATGTCTGTCTGCGGGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTGTCACTAATTTATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTGCACCTTTTGTGGCAATATTAAAGTGAAGTCTCTAATA GTGTAAGTATCTGTGTCACAAACCACTGCCAGATAACACAGAGGGGCTG
WI-7233	211 T C	...	CGATCGTACTGCCAGTAGCATGTCTGTCTGCGGGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTGTCACTAATTTATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTGCACCTTTTGTGGCAATATTAAAGTGAAGTCTCTAATA GTGTAAGTATCTGTGTCACAAACCACTGCCAGATAACACAGAGGGGCTG
WI-7238	128 T C	...	GCGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACATTTTGTCTTAGTCTTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTCTTCTGCGTT CTGTTTAAACAGAAATAAAGAGGTGTAGCTCTTTTCTCATTTCAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAACATTCAGTAGAACATTTTATTCCTA
WI-7252f	520 T C	...	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCCCTGGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTTGGAGCGTTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252e	552 T C	...	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCCCTGGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTTGGAGCGTTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252d	540 T C	...	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCCCTGGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTTGGAGCGTTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252c	552 T C	...	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCCCTGGGCTCGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTTGGAGCGTTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252b	540 T C	...	CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA

WI-7252a	520 T C	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTCCACATCGACAGCAGCCGCGGGGACAGAG GCTTGCCTGGCGCGCCAGCCGCCCCGCGCTGGGCTGGAGGCTGGCCCCGCTGGTCTCTGGTCTCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA
WI-7265m	252 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT
WI-7265l	231 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT
WI-7265k	121 T G	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT
WI-7265j	174 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT
WI-7265i	227 T C	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT
WI-7265h	80 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT
WI-7265g	170 T G	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATTAGTATTTTGTATTTATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAGATTGGCTTT

WI-7282b	159	GC	---	---	---	TGTCACCTGGCACATTCATTTCTCAGTTGAAGAGAGAAATTTGAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGTGAGTGTTCCTCACTCAAAATATGTCAACTNNNNNNNT AGGCCCTTTCATAAAACCAAACTG/CJTAGCAAGATGCAAAATGCATGGCAAACTCTGCGGTCCTCA GTTGGTTATCTGAATAGTGTCAACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	TC	---	---	---	CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATTAATCTCCCACTCCACTAC TCTCTCCTCCACTCATTTTCCT/CJTGTGCTTCTCTCTAATTCAGTGTTTGGAGGCTGACTTG GGGACAACGTATTTGATATTATGTCGTCTTCTCTCCCAATAGAGAAATAGATCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	AG	---	---	---	AACATATGGCAGTGTCTGCTGTTATAGTAGAGCGCGGTATGTTGGTGGAGCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG A/GJCGGTAGTAACATATGTTGGTGGGAACTATAATGATTTTGAAATTTACAGTGGACACAGCA ATCAAAATATGGACACATGAAGGGGGCAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7301e	94	TC	---	---	---	AACATATGGCAGTGTCTGCTGTTATAGTAGAGCGCGGTATGTTGGTGGAGCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG TGACGGTAGTAACATATGTTGGTGGGAACTATAATGATTTTGAAATTTACAGTGGACACAGCAA TCAAAATATGGACACATGAAGGGGGCAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7301d	138	AG	---	---	---	AACATATGGCAGTGTCTGCTGTTATAGTAGAGCGCGGTATGTTGGTGGAGCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACTATGTTGGTGGGAACTATAATGATTTTGAAATTTACAGTGGACACAGCAA TCAAAATATGGACACATGAAGGGGGCAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7301c	211	AC	---	---	---	AACATATGGCAGTGTCTGCTGTTATAGTAGAGCGCGGTATGTTGGTGGAGCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACTATGTTGGTGGGAACTATAATGATTTTGAAATTTACAGTGGACACAGCAATCA AATATGGACACATGAAGGGGGCAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7301b	182	CT	---	---	---	AACATATGGCAGTGTCTGCTGTTATAGTAGAGCGCGGTATGTTGGTGGAGCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACTATGTTGGTGGGAACTATAATGATTTTGAAATTTACAGTGGACACAGCAA TCAAAATATGGACACATGAAGGGGGCAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7301	88	GT	---	---	---	AACATATGGCAGTGTCTGCTGTTATAGTAGAGCGCGGTATGTTGGTGGAGCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG TGACGGTAGTAACTATGTTGGTGGGAACTATAATGATTTTGAAATTTACAGTGGACACAGCAA TCAAAATATGGACACATGAAGGGGGCAGTTTGGTGGAGAAAGCTCGGGCAG

WI-7301	205	A C	...	AACTATGCGAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGAGCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAAGTATGGTGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAACAGCAATCA AATTACJTGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49	GA	...	CTCTCTTTTCTTCAGATCTGCTCTGGTTTTAATTTGGAGGTCA/GA/JTGTCTACCTCACTG AGAGGGAACAGAGGATATGCTCTTTTGACGACAGTGAATAAAGTCAATTAATAAAGTCTCCAGG ATTCTTTGGACCCAGGAAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAACTTGTTTTT
WI-7314b	49	GA	...	CTCTCTTTTCTTCAGATCTGCTCTGGTTTTAATTTGGAGGTCA/GA/JTGTCTACCTCACTG AGAGGGAACAGAGGATATGCTCTTTTGACGACAGTGAATAAAGTCAATTAATAAAGTCTCCAGG ATTCTTTGGACCCAGGAAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAACTTGTTTTT
WI-7314	36	A G	...	CTCTCTTTTCTTCAGATCTGCTCTGGTTTTA/JG/JTGGAGGTGTCAGTTGTTCTACCTCACTG AGAGGGAACAGAGGATATGCTCTTTTGACGACAGTGAATAAAGTCAATTAATAAAGTCTCCAGG ATTCTTTGGACCCAGGAAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAACAAACTTGTTTTT
WI-7321b	199	C T	...	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAGGGTGGGTGTGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGGCTCCA GTCACTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC/C /TGTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGGCTGGCCA
WI-7321	199	C T	...	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAGGGTGGGTGTGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGAGTCTTTGGCATCCAGGGCTCCA GTCACTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC/C /TGTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGGCTGGCCA
WI-7336b	248	A C	...	AGACATCTCGCTTCCCTGAAGACTGAAGAAAGTGTAGTGCATGGGACCCAGAAACTGCCCTGGC TCCAGTGAAGACTTGGGCACATGCTCAGGCTACTATAGTCCAGAGTCTCTTATTAAGCCCTGGCAG GCAGGTGTTTAAATCTGAATTTTGGGGATTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTGTGATCAGATCTGGGCAGCAACCTATAAATCAJ/CJCA
WI-7338c	221	A G	...	CTCTTCTCAGCACATTGATGGCAACTAGAAATACAGCAGTTTCAACTCTACCATGGATAATGCA /AACAAACCGAAGCTACATGCCAATGATAGTGCAGAAATATGGCAAGGTGCTTTACCTTGAGC CATATTTGTGTACAGAAACAAAGAAACAGAAATCAATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTTTACACACJ/GJ/TATACACAGACATCAGAAATTTCTGT

WI-7338b	125 A C	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7338	125 A C	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7338	221 A G	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7384c	146 T A	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7384b	146 T A	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7384	145 T A	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7388c	106 A T	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT
WI-7388b	106 A T	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGCAAAAGGTCTTTTJACJCTTG AGCCATTATTGTGTCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAATTCGT

WI-7388	94	T A	TGAAATCCTGGGTCTCTGGCTGCTGCTAGCTGTTATTTTACTTTGCCCTCCACATTTTT TGAGATCCATCCCTTATCAAGAAATGCTGAAGCGACTATAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAAGTTTACCTCTATTTTGCACAAAGCGTCTCGGATTTGTTTGA CTTGCTGCTGCTCAAGAACTTTTCCCCCAAGATGTATAGTTATGG
WI-7438	64	A G	TTAGATTTTAATTGGCAACCACTCACTGCCACCATCCACTGCAGATCTNCTCTCTGGG/GJ GTTGATATGACAAAGAAACCTATTGGAACCAAGTCTTCAAGTTGNCATGTGCGACAGAGGCTCCT TGCTGTAGGTGTAGCATGTACACTGTACTGTTCAGTGTACATAGTTTGTGTCGTTATTTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T C	CCATGATCCCTCCCTCTTGCCAAATGGAGAAAGCTGTGGTGTACCAACAAAGCCCAACCC CAGTACAACTGAGATGAGAGAACCTGTAGACTGTCTGAATGCCAGGAGCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCATTGTCTACTTCTCAATGTTTTGACA
WI-7454	152	T C	CCATGATCCCTCCCTCTTGCCAAATGGAGAAAGCTGTGGTGTACCAACAAAGCCCAACCC CAGTACAACTGAGATGAGAGAACCTGTAGACTGTCTGAATGCCAGGAGCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCATTGTCTACTTCTCAATGTTTTGACA
WI-7464c	177	G C	AATTTGAAAATCTGAAAAAAGTGCTAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTCTCACTCAGTCCATCTTAACCATGTACAAATGCCTAAATTAATTTTCTATGTA CAACAGCCACAGCACAAGGGTGGGCATAGCAGTTGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAAAGCAACGTTACCAACAATAT
WI-7464b	168	C A	AATTTGAAAATCTGAAAAAAGTGCTAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTCTCACTCAGTCCATCTTAACCATGTACAAATGCCTAAATTAATTTTCTATGTA CAACAGCCACAGCACAAGGGTGGGCATAGCAGTTGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAAAGCAACGTTACCAACAATAT
WI-7464a	103	C A	AATTTGAAAATCTGAAAAAAGTGCTAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTCTCACTCAGTCCATCTTAACCATGTACAAATGCCTAAATTAATTTTCTATGTA CAACAGCCACAGCACAAGGGTGGGCATAGCAGTTGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAAAGCAACGTTACCAACAATAT
WI-7499b	134	T G	CAATTTCTCAATCCAACTAGTGTGCTTAACCATTCAGACAAAGTTCACATTCGAAAGGTTTA AATGCATAAGTCAGATAGCAATCCCTCAGTTGCCACAGAGGCATACGTTCTTTGAATGCTTCAT /GJTATAGTCCCTCTCAATTTAGCAATCAGTGAAGCAATACACTGGCATCATGCCCTTTTATAGGA ACTCTGTACAAAATTCCTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7576b	168 A T	---	---	---	AATGATGATGATGATGATGACGACGACAAACGATGCTGTAAACAAGAAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAGAGGGCTAGTGTTCAGACACTTTTGAAGTGTGTG TCTGTTTGTGTTAAACATGGCATCTGCACACAAAAAATGTTGTAAGGCGCTTATCTACATTTCCACCTAC TTTGTAGTGAGAGAGACGAAGAAGCAAAANNNNNNNNNAAAGAAAAAATAAC
WI-7577q	77 T C	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA AAATATGCATTC/CAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACTAT TGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577p	50 G C	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACTAT TGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577o	157 G A	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACT ATTGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577n	48 A G	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACTAT TGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577m	84 G A	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACTAT TGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577l	93 T C	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACT ATTGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC
WI-7577k	154 C A	---	---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AGAAAGTTCATTTGGTTACAGTAGGAAGAAGAGACATCAAAAGTGAGATATGTTAACT ATTGTAATGTTGGCCTGTTATACATGACACTCTCTGAAITGACTGTATTTC

WI-7577j	117 A G	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577i	77 T C	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577h	50 G C	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577g	157 G A	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577f	48 A G	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577e	84 G A	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577d	93 T C	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC
WI-7577c	154 C A	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTTATACATGACACTCTCTGAAITGACTGTAATTC

WI-7577b	117 A G ...				AACCATGTTCCCTTC TCTAGCACCAAAATATCAAAACCAACATAAGTGTTCCTTTTAA AAATATGCATCAAAATGCTCTCTCATTTCTCTGAGGGTTTAGTAAAGACAGTAGGATTAAT AAAGAAATTCATTTGGTTTACACGTAGGAAAGAGAGACATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACCTCTCTGAAATTGACTGATTTTC
WI-7577	107 G A ...				AACCATGTTCCCTTC TCTAGCACCAAAATATCAAAACCAACATAAGTGTTCCTTTTAA AAATATGCATCAAAATGCTCTCTCATTTCTCTGAGGAGTGTAGTAAACAGTAGGAGTTAAAT AAAGAAATTCATTTGGTTTACACGTAGGAAAGAGAGACATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACCTCTCTGAAATTGACTGATTTTC
WI-7619q	106 C G ...				ACAAAGGCGACTTGAAGAGGAGCGAGGCTTCCAGAGGACAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619p	150 T C ...				ACAAGGCGACTTGAAGAGGAGCGAGGCTTCCAGAGGACAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619o	228 A G ...				ACAAGGCGACTTGAAGAGGAGCGAGGCTTCCAGAGGACAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619n	237 G C ...				ACAAGGCGACTTGAAGAGGAGCGAGGCTTCCAGAGGACAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619m	99 C T ...				ACAAGGCGACTTGAAGAGGAGCGAGGCTTCCAGAGGACAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619l	189 T A ...				ACAAGGCGACTTGAAGAGGAGCGAGGCTTCCAGAGGACAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619k	90 C	---	---	ACAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCATCCGCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTAC ATGCGAGGAAGATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT CGCTTGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG ATGGCAGGAAGATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT CGCTTTCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG TGGCAGGAAGAATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCGCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G	ACAAGGCGAC TTGAAGGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAGGCCCAATGGGTCATCQCGTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGCCCTTAAGGGAGTGTGGGGTGTGCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G	ACAAGGCGACTTGAAGGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAGGCCCAATGGGTCATCQCGTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGCCCTTAAGGGAGTGTGGGGTGTGCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCT/GTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A	ACAAGGCGACTTGAAGGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAACAGAC AGAGAAGGCCCAATGGGTCATCQCGTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGCCCTTAAGGGAGTGTGGGGTGTGCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCAGTAAACCAATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCAAAATTTAGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTATTATAGTAAACCAATTTTCTTTGGACTGTTCA
WI-7626c	155 C T	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTTTAAACCAAAAGCAACAGTAA TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCAGTAAACCAATCATGGACCAATGTG TACTAATGATGAGCAATTTAGC/TACAAATTTAGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTATTATAGTAAACCAATTTTCTTTGGACTGTTCA
WI-7626b	28 T A	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCAGTAAACCAATCATGGACCAATGTG TACTAATGATGAGCAATTTAGC/TACAAATTTAGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTATTATAGTAAACCAATTTTCTTTGGACTGTTCA
WI-7626	144 T C	TCCCATACCGCTGATCTCAGGCTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCAGCAGGTGGGC TCCCATACCGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAGGTTGTTCTTAA /GTTAAGGCGAGAGTCACACTGGGGCAGCTGATACAAATTTGACACTGTGTAAAGAGAGCCTTAAT GATAATATTGGTGGCGCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689c	134 A G	

WI-7689b	134 A G	TCCATAACCGGTGATTCACGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGCGAGCTGATACAAAATTGCGAGCTGTGTAAAAGAGAGCTTAAT GATAATATTGTGTGGTCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A	TCCATAACCGGTGATTCACGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTGTTCTCTAA AATAAGGGCAGAGTCACACTGGGCGAGCTGATACAAAATTGCGAGCTGTGTAAAAGAGAGCTTAAT GATAATATTGTGTGGTCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A	TGGGAACATTCATCTTGGCGTCACCTATTCAATGAAGATTAG/ACACTGAGATCCAGAGAGG CTGGATGACTTGTCTCAAGTTCACCCAGCATGGTAGTGCGAAAGAGGTCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACGTGCAGTTCATCC
WI-7703b	164 T C	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATGGAAACAAGTCAGTCAATCAGATATGATTCAAA TGCTATAAACCAAACTGATGT/CAAGTAAATGGTCTCTCAGTGTGTTTATTAACTCTAAATTTCT TTCATTTTAGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C	TAAATGAGTGTGTTGTCAACGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/ACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAACTCTGCTACCTCAGTGGGCTCTGGGCTGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCCAGCTCTCAGCC
WI-7743e	106 C A	TAAATGAGTGTGTTGTCAACGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/ACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCAGTGGGCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAAGACAGCCGCTCTGTCTGCCAGCCAGCCAGCTCTCAGCCAAAG
WI-7743d	275 C T	TAAATGAGTGTGTTGTCAACGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/ACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAACTCTGCTACCTCAGTGGGCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCCAGCTCTCAGCC
WI-7743e	106 C A	TAAATGAGTGTGTTGTCAACGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/ACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAACTCTGCTACCTCAGTGGGCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCCAGCTCTCAGCC

WI-7743d	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106 C A	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743d	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743c	106 C A	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743b	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	106 C A	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTCGGGTCTGGGGCTCGAGGCTCCTCGAGGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7758	144 A G	...	TGACATTATTCAGAGTTAAAGCAACACTTACAGAAATTAAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTCAGAGAGCTCGTAAATTAAGCAACAGAGTACATCATCAAGTG GAGAGAAATC(A/G)TAGTTTAACTGCATTAAATTTTAAACAGAAATTAAGTAGATTTTAA GATAAATGTGTAATTTGTTTATTTTCCATTTTGGACTGTAAGTACTGCCC

WI-7765b	126	G C	ACAGGCGCTTTGCGAGGTGCAGCCCCACCTGCTTTGAOCTGCCCTCCCTTCATGATGAAATTCOCT TCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAGGAGGTGAGTATGG(GC)ITAGG GAAACATTCACCTCTGAGTCAAAAATCTCAATCTTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAACCAATCAGTAACTTTGCTGAGCCTGTAAATAAAGGTCGGA
WI-7773b	237	C G	TTAATTTACTGATCCAGCAGCAACCAATCATTTGATCAGATTATTTTAAAGTTTATCCGTAAGTTT GATAAAGATTTCCTATTCCTTGGTCTGTCAGAGAACCTAATAGTGCTACTTTTGCCATTAAGGCA GACTAGGGTTTCATGCTTTTACCCCTTNNNNNNNNITGTAAAGTCTAGTTACCTACTTTTCTTT GATTCGACGTTGACTAGCCATCTCAAGCA(C)GTTTCGACGTTTGA
WI-7774b	170	T C	TGCAACCTCTTTCGTGATGGGCGCCTGCTGGTCAGCACTCCAGTAGCGAGAGCGGCCACCCAGAT CAGATCCACGCTTCGGCATTTGATCAGACCAACAGCTGCTTTCCCGGGGAGGAAACACTTTTAA TTACCTTTTGAGGCGACCCCTTAACTCTTTT/CJATACCTGCTTTAATAATGAGCGACTTAAA ATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGC
WI-7785c	165	G	GCAGAGACCTTCCAAGGACATATTGCAAGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATCTGTAATGCAATGGAATAAACTGTCTCCCTCATGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAGGCTAATCCAAATTATTATATCACATTTACCA TAAITTTTGTCCATTGATGATTATTTTGTAAATGTATCTTGGTCTGC
WI-7785b	165	G	GCAGAGACCTTCCAAGGACATATTGCAAGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATCTGTAATGCAATGGAATAAACTGTCTCCCTCATGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAGGCTAATCCAAATTATTATATCACATTTACCA TAAITTTTGTCCATTGATGATTATTTTGTAAATGTATCTTGGTCTGC
WI-7785	156	T	GCAGAGACCTTCCAAGGACATATTGCAAGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATCTGTAATGCAATGGAATAAACTGTCTCCCTCATGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAGGCTAATCCAAATTATTATATCACATTTACCA TAAITTTTGTCCATTGATGATTATTTTGTAAATGTATCTTGGTCTGC
WI-7789c	84	G A	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAGGAGGGCCACCATCTACAGAGACTCTCC TGACGGTGGAAITTAAG(A)TTAGGGTCCCTAAAGCATTTGACACACAGATTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGCTCAGACGACTAGCCAGGACCATCT
WI-7789b	84	G A	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAGGAGGGCCACCATCTACAGAGACTCTCC TGACGGTGGAAITTAAG(A)TTAGGGTCCCTAAAGCATTTGACACACAGATTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGCTCAGACGACTAGCCAGGACCATCT

WI-7789	73	GA	---	---	---	TCTCCCTCATCACTCCGAAAGTCTGAATCTCCCAAGGAGGACCATCTTACAGAGACTCTCCC TGACG[G]GTGAATTTAAGTTTAGGGTCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190	CT	---	---	---	AATGTCAGTCACCTTTCAAAACCTTACAGTCTTCTTAAGGTTACTCTTCATGAGATTCATCAAT TACTAATACCTGATTTTGGTGGACTAGGCTTGCTATGTGCTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTCTATTCTTGAACCTC/TCTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	CT	---	---	---	AATGTCAGTCACCTTTCAAAACCTTACAGTCTTCTTAAGGTTACTCTTCATGAGATTCATCAAT TACTAATACCTGATTTTGGTGGACTAGGCTTGCTATGTGCTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTCTATTCTTGAACCTC/TCTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	CA	---	---	---	CAGATGTTCTGGTAACTGATGCTGGCAACAGATCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[CA]GTCATCATCAAGAAATTAATGATTAAGTAAATAGCATGCCCTTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAATTTCTCTGAGGAAAATGTGCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81	CA	---	---	---	CAGATGTTCTGGTAACTGATGCTGGCAACAGATCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[CA]GTCATCATCAAGAAATTAATGATTAAGTAAATAGCATGCCCTTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAATTTCTCTGAGGAAAATGTGCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41	GA	---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGATTTTCAITTAGTCAITGTGACCCTC TGCTTTGTGTTTCCAGGCTGCAAGTTGAGTCCAGGATGCTACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGATTTC TTTCTTTCTCTGGTAAATTTGACTTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41	GA	---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGATTTTCAITTAGTCAITGTGACCCTC TGCTTTGTGTTTCCAGGCTGCAAGTTGAGTCCAGGATGCTACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGATTTC TTTCTTTCTCTGGTAAATTTGACTTTGATATTTTAAAGAAATAACAGAA
WI-7814	28	GA	---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGATTTTCAITTAGTCAITGTGACCCTC TGCTTTGTGTTTCCAGGCTGCAAGTTGAGTCCAGGATGCTACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGATTTC TTTCTTTCTCTGGTAAATTTGACTTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	...	GCAGAAATAGTCACTCATCCACATCCACATAAGGGTTAGTAAAGAGAGTCTGTCTGTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCAATCATCATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGTC/CTTTAATGTACACATTCGCAATTTGATAAAATTAATTTTGTTCCTTTTG AGGTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTTCCGTTGGGA
WI-7830c	54	G A	...	GCAGAAATAGTCACTCATCCACATCCACATAAGGGTTAGTAAAGAGAGTCTGTCTGTGATGA TGATGGATAGGGGCAATCTTTTCCCTTTCTGTTAATAGTCAATCATCATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTTAATGTACACATTCGCAATTTGATAAAATTAATTTTGTTCCTTTTG AGGTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTTCCGTTGGGA
WI-7830b	134	G A	...	GCAGAAATAGTCACTCATCCACATCCACATAAGGGTTAGTAAAGAGAGTCTGTCTGTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCAATCATCATTTCTATGCCAAACAGGAAC G/ATCCATAACTTTAGTCTTTAATGTACACATTCGCAATTTGATAAAATTAATTTTGTTCCTTTTG AGGTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTTCCGTTGGGA
WI-7830	44	A G	...	GCAGAAATAGTCACTCATCCACATCCACATAAGGGTTAGTAAAGAGAGTCTGTCTGTGATGA TGATGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCAATCATCATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTTAATGTACACATTCGCAATTTGATAAAATTAATTTTGTTCCTTTTG AGGTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTTCCGTTGGGA
WI-7865e	25	C T	...	CCACTTCCTATCTGATTTTCCCAAGCT/AAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTGAGGGTGTCTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCAGATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	...	CCACTTCCTATCTGATTTTCCCAAGCT/AAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTGAGGGTGTCTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCAGATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	...	CCACTTCCTATCTGATTTTCCCAAGCT/AAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTA ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAGATTTGAGGGTGTCTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCAGATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	...	CCACTTCCTATCTGATTTTCCCAAGCT/AAATGAGGCGAGGCAATTCAGTCTTCCACAAACATCTA ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAGATTTGAGGGTGTCTCCCACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCAGATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T	CCACTTCCTATCTGATTTTCCAGGCTAAATGAGGCGAGGCAATTCAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTCAGGGTGTCTTCCAACTGAATCTCAATGTCTCAGTACGAAAAAC CTGAAATGCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCCAA
WI-7865	191 C T	CCACTTCCTATCTGATTTTCCAGGCAATGAGGCGAGGCAATTCAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAATCTCAATGTCTCAGTACCTGAAAC CTGAAATGCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCCAA
WI-7867c	92 A C	TTCAACACCTGTCTCCACCTCCACCATCTGTGCAATCATCTCACCCTCGCCCTCAGTCTAGTCCCC CTAACAAATACCTGTCAAGAGGACGAGTGCAGTGCAGTGCAGTGGATTAAATGTGGGTTAAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTAAAGTAAACCATTTCTGTTCTGCTATAAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C	TTCAACACCTGTCTCCACCTCCACCATCTGTGCAATCATCTCACCCTCAGCCTCAGTCTAGTCCCC CTAACAAATACCTGTCAAGAGGACGAGTGCAGTGCAGTGCAGTGGATTAAATGTGGGTTAAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTAAAGTAAACCATTTCTGTTCTGCTATAAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T	TTGATCGATCTTTCCACCTGTCACTCAAGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CAACCAACCTGCTCCCTCTGATCCTCCATCAGGCGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAACCTTGAAGGCGCCAGAAAATGGGCAAAATTAT CACTACAGGCTTTGACTCAGGTTCCAGTAGTTCATTTCTAATGCTAGAT
WI-7868b	173 C T	TTGATCGATCTTTCCACCTGTCACTCAAGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CAACCAACCTGCTCCCTCTGATCCTCCATCAGGCGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAACCTTGAAGGCGCCAGAAAATGGGCAAAATTAT CACTACAGGCTTTGACTCAGGTTCCAGTAGTTCATTTCTAATGCTAGAT
WI-7868	66 T C	TTGATCGATCTTTCCACCTGTCACTCAAGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CAACCAACCTGCTCCCTCTGATCCTCCATCAGGCGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAACCTTGAAGGCGCCAGAAAATGGGCAAAATTAT CACTACAGGCTTTGACTCAGGTTCCAGTAGTTCATTTCTAATGCTAGAT
WI-7870b	85 T C	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAACACTATAATACTCTGCAAGTATTAGAGGG GTGGGTGGGGGAATCCTTCATTTATCAGACTCTGTAATTTGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTTGCTGCAAAATGAATCCAAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCATCAATTAACAGCTGTAGACCCACCTAATATCAATTTG

WI-7870	76 C T	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTCGCAGTGAATTGAAGGG GTGGGGTGGGCTGGGAAATCTCTATTCAGACTCTGTAATTTGAATATAAATGTTTACTCAGAGGAG CTGCAAAATTCCTGCAAAATGAAATCCAAATGAGCACTAGAAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGACATCAATTACAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C	---	---	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGGGCGCTCTCCCGCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCCCTCT GAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCCCTCT TGCTCCCTGCCCAATCTCCCTCGGAGAAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAAGGCTGTCTCCCGAGAGCAAGAAAG
WI-7889b	54 C	---	---	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCCTGGGGGGGCGCTCTCCCGCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCCCTCT GGCTCCCTGCCCAATCTCCCTCGGAGAAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAAGGCTGTCTCCCGAGAGCAAGAAAG
WI-7894c	142 A G	---	---	AGCCACGCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCATACATCAATTAACATTTAGTCTATGTTTGTGAAATTTATTTGGGTATAC ATTATCAGTATGTAAATTTGCAATTTTTTATTGAAATTTGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACGCTATAGAGTATTCGATA
WI-7894b	142 A G	---	---	AGCCACGCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCATACATCAATTAACATTTAGTCTATGTTTGTGAAATTTATTTGGGTATAC ATTATCAGTATGTAAATTTGCAATTTTTTATTGAAATTTGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACGCTATAGAGTATTCGATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCATCCTTACTCTACTTGGCCAGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCAACTGGCCATGCTGCTGCAATTAACAGTGAATTTGATCAAGCCATGGTGACACA AAAATGCATTTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCATCCTTACTCTACTTGGCCAGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCAACTGGCCATGCTGCTGCAATTAACAGTGAATTTGATCAAGCCATGGTGACACA AAAATGCATTTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAGAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCATCCTTACTCTACTTGGCCAGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCAACTGGCCATGCTGCTGCAATTAACAGTGAATTTGATCAAGCCATGGTGACACA AAAATGCATTTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAGAAGAAATC

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTAGTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTAGTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTAGTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTAGTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTAGTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900	84 C T	---	---	AGACTTAGGTACAATTCGTCCTCTCTGTCATACAGACAGGTAAACCTTAGTCTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7901c	33 C T	---	---	AGACTTAGGTACAATTCGTCCTCTCTGTCATACAGACAGGTAAACCTTAGTCTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7901b	33 C T	---	---	AGACTTAGGTACAATTCGTCCTCTCTGTCATACAGACAGGTAAACCTTAGTCTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACAGTGAATTAAGTTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAAGACATTTAAAGAAATC

WI-7901	33 C T	...	AGAC TTAGGTACAA TTGCTCCCTTTTATATAC/TJAGACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTTGTTGGGTCGCTGGTTATTTGGGGCAGCGCGGTGGTCTGT CACTAGTGGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACTAGTTCT
WI-7901	271 T G	...	AGACTTAGGTACAA TTGCTCCCTTTTATATACAGACACACAGGACACATATATTAAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCT TTTAAACAACTCCAGGCCCTTGTTGGGTCGCTGGTTATTTGGGGCAGCGCGGTGGTCTGTAC TCAGTGGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACTAGTTCTGTGT
WI-7926c	150 C A	...	CATTCCGATCTGTCAACAGGACAGAAAGCATGGACAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAGCAAGTGTATACAAACAGTATTTGGGAATGCCTTCATT TACAAATGCAATACTTACATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTTATACAGAAATTACACTGTGGAA
WI-7926b	28 A T	...	CATTCCGATCTGTCAACAGGACAGAAATJGCAATGGACAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAATTCATATTTAGCAAGTGTATACAAACAGTATTTGGGAATGCCTTC ATTACAATGCAATACTTACATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTTATACAGAAATTACACTGTGGAA
WI-7926	150 C A	...	CATTCCGATCTGTCAACAGGACAGAAAGCATGGACAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAGCAAGTGTATACAAACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTACATTTTAACTCTTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTTATACAGAAATTACACTGTGGAA
WI-7947b	203 G T	...	AAGGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCAGAGGTCACTCTTTACAGTTAGAACACAGCCGAGCCACAGATCCCATCCCTTTCC TGAGTCATGGCTCAAAAATCAGGCCACCATTTGTCCTCAATTCAAATCCATAGATTTCGAAGCCACA GAG/TJCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGCTGTGCACTG
WI-7947	203 G T	...	AAGGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCAGAGGTCACTCTTTACAGTTAGAACACAGCCGAGCCACAGATCCCATCCCTTTCC TGAGTCATGGCTCAAAAATCAGGCCACCATTTGTCCTCAATTCAAATCCATAGATTTCGAAGCCACA GAG/TJCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGCTGTGCACTG
WI-7963b	145 T C	...	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAATGCC ACAAATTCATTTCTCTCTTAAGTATTACAAATGGAGTTTCTCTGCCTAAAAAGTGGAGAAAT TGAGTGAATGAT/CJAAATTTTGTAAATTTAGGATAAGATCCAAAGTATTTTCCCAACTCTGTTCCTCC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAAGGCAGAGCGGAA

[illegible]

WI-8021b	57 C T	ACAATCTCAGAGGACTGTGCAAGTCAATGAGTCGCTGTGAAATCTCATCTGGAAAC/CTGATCCC ACGCTTTAGAACCTTACCACAAAGGAGTTTCTTGTAGTGAATCTCAAGTCTCAAGTCTTGGTAGGCATTGGA ACTGGTCTTTCACCTTGGAGATTCTTCTTTCGGCTCTTATCAAGTCAAGTCAAGTCAAGTCTTTCOAAG GATTTACGTTCGGCTTGTAGGGTGAATCGAATTCGGTGAATGCGA
WI-8021	57 C T	ACAATCTCAGAGGACTGTGCAAGTCAATGAGTCGCTGTGAAATCTCATCTGGAAAC/CTGATCCC ACGCTTTAGAACCTTACCACAAAGGAGTTTCTTGTAGTGAATCTCAAGTCTCAAGTCTTGGTAGGCATTGGA ACTGGTCTTTCACCTTGGAGATTCTTCTTTCGGCTCTTATCAAGTCAAGTCAAGTCAAGTCTTTCOAAG GATTTACGTTCGGCTTGTAGGGTGAATCGAATTCGGTGAATGCGA
WI-8024c	206 A G	CTGAAATTTACTATGCTCTCCACAAACAGAGCTCCCATTTTCCACAGACACAGTCAATGTGATGCA GCTTGTATTCAGGAGGACAGGGGAGGAGTCCAGTGGCACTTCCATGGGAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAAACCAATTCAGCCGCTTAGCCTCTAA TTCCGAGCTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGGAAAGAGC
WI-8024b	206 A G	CTGAAATTTACTATGCTCTCCACAAACAGAGCTCCCATTTTCCACAGACACAGTCAATGTGATGCA GCTTGTATTCAGGAGGACAGGGGAGGAGTCCAGTGGCACTTCCATGGGAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAAACCAATTCAGCCGCTTAGCCTCTAA TTCCGAGCTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGGAAAGAGC
WI-8077	187 A G	GAATGAGCCTTCTAGCGCGAGGACCTGCTGCTGTGTTGGCCCTGCACATGCAATCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCAAACTCCTTCT AAGGAGTCTGGGGTGTATGCCCTACAAACGAGTAAATCTCATGATGGAATTTTAACTGTT GTGATGTGACTTACTTTCCAACTGACTCTGGCATAACAAAGGAAAGAGC
WI-8118f	114 G C	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGTAAAGGAGCTAT GTACTTCATGCTGTGAAACTGGCAATACAGAAATGATGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCTTGTGACCAAGTAGTCTTGGAGACTCAAGCTGAATGA
WI-8118e	40 A G	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGTAAAGGAGCTAT TATGTACTTTCATGCTGTGAAACTGGCAATACAGAAATGATGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCTTGTGACCAAGTAGTCTTGGAGACTCAAGCTGAATGA
WI-8118d	118 T G	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGTAAAGGAGCTAT GTACTTCATGCTGTGAAACTGGCAATACAGAAATGATGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCTTGTGACCAAGTAGTCTTGGAGACTCAAGCTGAATGA

WI-8118c	44 C T	<p>TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGAATGA(C)TCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAAATAGCTGTGTTTCTTAGCCTTGAAGA TGACCAAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTTATTCCTTCT AAAAATCAGACTCATTTGACCAAGTAGCTTTGAGGACTCAAGCTGAATGA</p>
WI-8118b	88 T C	<p>TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTTC/GGCAATACAGAAATAGCTGTGTTTCTTAGCCTTGAAGA TGACCAAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTTATTCCTTCT AAAAATCAGACTCATTTGACCAAGTAGCTTTGAGGACTCAAGCTGAATGA</p>
WI-8171d	299 C T	<p>TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAACTGGCAGCGGCTCGGGGAG AGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACAC TTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAATGGGCAAGAGACCAATGAAGAGGATGATGATATAAAACAATCACGGCA</p>
WI-8171c	46 A G	<p>TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAACTGGCAGCGGCTCGGGGAG AAGAGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAAGTGGGCAAGAGACCAATGAAGAGGATGATGATATAAAACAATCAC</p>
WI-8171a	46 A G	<p>TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAACTGGCAGCGGCTCGGGGAG AAGAGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAAGTGGGCAAGAGACCAATGAAGAGGATGATGATATAAAACAATCAC</p>
WI-8171b	298 T C	<p>TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAACTGGCAGCGGCTCGGGGAG AGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACAC TTATGGAGGGTTGCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACCAATGAAGAGGATGATGATATAAAACAATCACGGCA</p>
WI-8314b	85 G C	<p>GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTTAAGGG(GC)GAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCAATAGAACTTTC TGATGATGAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT</p>
WI-8314	78 C G	<p>GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTTAAGGG(GC)GAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCAATAGAACTTTC TGATGATGAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT</p>

WI-8450g	55 T C ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450f	108 T A ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450e	125 T C ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450d	125 T C ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450c	108 T A ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450b	61 C A ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450a	55 T C ...			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACATCCCAT CTCTATCTTAGTCCCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60 A G ...			CAAGGAAAGCTGTGAGTCTTCATAAATTTCAAGAGTTTACAAAAATACGTTATTTTAA/GICTA CAATTCAGGATAGCATCCAAACCTACAAAGATGATGATACATTCGTACACACCATACACCTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTACATTTGTTGAAACCTTTATTTGTCACAGT GACATCCATTCGCGCAGACTTAATGTTTAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTGAGACAATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTTTTATJNNNNNNNNCTTGCTTATTTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTACAAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461b	38 T C	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTGAGACAATTCJATAACTACAACCTTACAAATGCCAA TTAGACAAGAGANTAAATGATATAATATAATCATTTTTTNNNNNNNNCTTGCTTATTTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTACAAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461	38 T C	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTGAGACAATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTTTTJNNNNNNNNCTTGCTTATTTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTACAAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461	105 A T	---	---	CTTCCTCCTCCAAAATCTACATGAATACCTGAGACAATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTTTTJNNNNNNNNCTTGCTTATTTCACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTACAAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-9438	77 A G	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGGTAGATGACTTAATTTTTTGATAAAAAAT TAAAAAGCATJGJAACATGCATATAAAAAATAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATTCTCCCTTTGTTTTGCTTTTTTAAAAACATTATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAGAAATTA
WI-9439b	101 C T	---	---	ACAGAAATGACCTTTATTTGTTGTACTAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAATCCAGTCTGTGACGTCAGTACCTGTCJTGTCACACTGTACCATCTCAGTCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAACTCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAAAACAAG
WI-9439a	76 C T	---	---	ACAGAAATGACCTTTATTTGTTGTACTAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAATGTCAGTCTGTGACGTCAGTACCTGTCGTGTCACACTGTACCATCTCAGTCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAACTCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAAAACAAG
WI-9446b	75 T C	---	---	GAAAGCCTTGATTAAAGGAGGNTTATTTGATTGTAACCTACCATTCCATAGACTATAAGANCATTA TAAAAAATTCJCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGTCNCCCTACTNTATCACTGTGCTTCTGCTTTGCTGTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75	T C	---	GAAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACCTACCATTCATAGACTATAAGANCAATTA TAAAAAATTCCTCTAAAGNGACACATGCCCCAAATGACANGNCATAAAGCAACCTTTTAAAT TACTCATCTTCATATGTGTGTGTCNCCCTACTNTTATCACGTGTCTCTGCTTTTGCTACCTA TGNGAAGCTGCACACTATCTGTGGCAATATGT
WI-9497b	185	A	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATCTTTTTT GAGATAATTATTCTAGATCCAGGCTTCTCTAGATGTAAGTAAAGCTTAAGCTTAGTTTACATTGA TATCTAGACATATATCTAAACAGTCTCCAAATTTNCCTTTAAATTAATCAAAAGTATGTTAATGTACATT GGAATTCATACATGGAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9497	185	A	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATCTTTTTT GAGATAATTATTCTAGATCCAGGCTTCTCTAGATGTAAGTAAAGCTTAAGCTTAGTTTACATTGA TATCTAGACATATATCTAAACAGTCTCCAAATTTNCCTTTAAATTAATCAAAAGTATGTTAATGTACATT GGAATTCATACATGGAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9523b	193	C A	---	GTGAAAAAGTTTCTATTCTATCCATCATCAATAGATTGTGCTAAGTATCTTTTGGAAAGATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCACTGCACTGCAAGCTTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTATTTCCACACATTGTATCAAGTG AAGCTCTTCAGCTTGGAAACAACTTGTCAAGGCGAGCTGCATGCACATATAT
WI-9523a	47	GA	---	GTGAAAAAGTTTCTATTCTATCCATCATCAATAGATTGTGCTAAGTATCTTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCACTGCACTGCAAGCTTTTATCTAAAGTACGTGC CAGACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACTTGTCAAGGCGAGCTGCATGCACATATAT
WI-9554	202	T C	---	AAAAACAAAGTTTCTATACATCACAAAAACCTTCCATTATACACAGAAAGTGATTATACCAGAC AAGCATCAGTGATGATCTACTGCCCTTTCCTAGTTGTTATTTGTAAGTCTAGATAATGCAGCCCATG CAATACCCCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAGCGACGCCCTCTGCAAGTG GTTCTGCTGGATACCACTAAGAAAGTCTACTGCAGCCCATGTTGGTTATGATTTT
WI-9555	97	GA	---	CCAAAGCCCAACCACTTATGTTGATGTTTCAATAACATTTATGATCCCTTTTGGAGTAAGTAT AAATACCTTTTACATGGCTACCTTCTAAGTATGTTTGAATAATCAATTTCAAGGACTCTTTAATCA GTTAAATATCTGCTTTAGAAGGCCAATAATGATCATCTCAGATTAAATATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAGGCTGTAACTCTTTTTCACATGATCACA
WI-9625b	172	A T	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACATAGCTACCATATATTTGTATCTNCTCTTGGGAAAAACCTTTGGAAAAAAGAACACGCACA TAAGTATCACTAAGCTGAGGGTTGTGGACAAGTTACTTCTATGTTTACCCTTTTATTTTATTTGACATAA AGTAGCACAGACTAGTTTTCATTTAAAAAACACACTGACAAATCTCTTTC

WI-9625	172 A T	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCTTGGAAAAACCTTTGGAAAAACACACGCACA TAAGTATCATAACTGAGGGTTGGACAAAGTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCAGACACTAGTTATTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTCTACTATACCTTTTTCATCCCTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAAGCT TACAACTTC/TGTCTTTTACCTGATACATTTATCCATTTACTTTTTCATTTGGAATTTTAAAAATGTTA ACTAATACGCTCTCTCAGATGTCCTGCTTTTAAATGTTGTTT
WI-9676n	114 A G	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTGCCC CCATTTACCTCAAGGCATCTTACGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTGCCCC ATTACCTCAAGGCATCTTACGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTGCCCC CCATTTACCTCAAGGCATCTTACGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTGCCCC ATTACCTCAAGGCATCTTACGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTGCCCC CCATTTACCTCAAGGCATCTTACGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTGCCCC ATTACCTCAAGGCATCTTACGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134 C A ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ C/AATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTG AGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676g	202 C T ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGAGGQ C/TGAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676f	184 G T ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676e	173 T C ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676d	134 C A ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ C/AATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTG AGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676c	114 A G ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676b	92 C T ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676a	84 A C ...	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT

WI-9738b	40 C A	---	---	---	TGGACCAACACAGACAGATGTAATCTGGTGGCCTGTGTA/C/AJATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGGTGGAGGGGGTGTTCCTACTATGTGAGTACTA TC.TTTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATGCTGTC
WI-9738	40 C A	---	---	---	TGGACCAACACACAGACAGATGTAATCTGGTGGCCTGTGTA/C/AJATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGGTGGAGGGGGTGTTCCTACTATGTGAGTACTA TC.TTTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATGCTGTC
WI-9756	47 A	---	---	---	ACTGAATGTAATGGCCAGGCACCCAGGACCTTAAATATCAAGAAGTTAATCTGTGGGAAAA GAGTAACATAACAAAAGCATCTAACAGAGCAGGATGTGATGATGTCCTCCCTTATCCTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGGATCCACTCCACAAACACACAGATATACACTTTTGAAG ATTCCACTTAACCACTTGATCTCTAC.TTTTATGATTTAAACTCTCCGTGG
WI-9758	135 A G	---	---	---	GATGGTCCCTTAAGGATTGCAATGGTAAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAGAGAAATTCCTGTCSCAAGGTCAATTTTATACATTTA A/GJTAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTCTAAAT ATTACG
WI-9778	127 G A	---	---	---	ATTTAAATCCAGCGAGCGGGAATAATGATACTTTTCATATGCTCTGTACCCAACTATAAACTTTTG GTTCTCATGACCATTTCATTTTGGCTTCTCACTCCAGTACCCTGATTTTACCAATTTGACTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAAATGTTGAAATTTCTCTATTACACACTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A	---	---	---	TCTCCCTTGGCTCTCTATGCCACTCCCTCAGCTGCACAGCGGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCCTGAGGACTTGTGCAATGCAATTCCTC/AJTTGGATCCCAAGGGA CTCAAAAACACTAGGAAATGGGAGAAAGGAGGACCTGGAAATCGGTGTGTAGCAAGCCCCAGGTGG TTTGTAGTGGACTAAGTTTGGAGCCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G	---	---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAAAATGGCATGA TATGAAATTCCTTTTGAATGAATAAATATAC/AJTTGTGTATGATATATATCTATTAAACACTT AGGATTATACACACAATAAAGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGATATGCTGTTG
WI-9880c	222 G A	---	---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTAATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCTTGGACTATAGATCTCTTTTAAATTTATTTTATATAAGCAGCATGAA AATGGAATGAATAATGA/GJA/TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ...	GAACCTAACACCTTCTTCGATGATTTTCTTGATTTAGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/CATATATAAGATCCTCTTTAAATATATATTTTATATAAGCACAT GAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ...	GAACCTAACACCTTCTTCGATGATTTTCTTGATTTAGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGAGTATATAAGATCCTCTTTAAATATATATTTTATATAAGCACAT GAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ...	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTCGGAATCAACTAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAACCAACGCCAGTTATCACAGTTTCTTNTTTTGTCTTCACC ATTTTCCATAACAAAGAGCTACACAAAATNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGTGCATGAATAATGATTCGAAA
FB25G10b	109	A G ...	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAAGAAATACTTTATGCCATTGTGATTAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAAATGGAA/GTGGATTTTAGATCCTCCGCCAG TGACAAGTAACTGAACTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G ...	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAAGAAATACTTTATGCCATTGTGATTAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAAATGGAA/GTGGATTTTAGATCCTCCGCCAG TGACAAGTAACTGAACTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A ...	ACAACGCTGAACCTCCATACAGTCAATGGTACAGTCAACACATCACATGTACAGAACACACAATTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT/CACAAATTCAGNAAACAAAAATCAAAAC ATTAAGNTCCCTGNNATATCTTAAACCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTACAAATATGACCTATTAAACCCAGTCTAGGGATCTG
NIB551	161	C T ...	CGTCTTCTCTTTTGGATGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGTTGTCCC TACTGAGCTTGGGCCAGGTGTGACTTAGGAACCCACCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCTCTTGAACACATACATGCGGCCATTGGTTGATTTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGCC
S72904	51	G T ...	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTCCCTTT/GTAAATTTGTCAGTTC ATTCCTGGAAAACTTTTGGATTAAATAAGGATCCTAGGACAGCACCTCGAAGTACAGGCCCTAAA GAGAAATTTGCTCAAAACCAACAGTGTGTAACCTCTCCCTTTCTGTCAATTGGTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	TAATCTTTTATCCTGGGCCACAGTCTTGATTATTCCTCTGTGGTAAAGACTGAATTTGTAACCC CAATCAGATAAATGGCAGTACTTTAGGACACACACAAACACAGACCTTACACCTTTTGATATGTA AGCTTGACCCTAAAGTCAAGGGACCTGTGTAGCATTCAGATTGAGC
ESTC1	33	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	GCTACTACACCGGCTGCTTGGTGGACAAAAATAACNAGGAGGATCCACGGGATTAGTTA GCCATCAAAATTCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC103	21	---	TGCTGGCTCAGTCTCCTCACANGCTGTATTACCTTTACAGAGCTGAGTGAGGCTGTGCT
ESTC107	20	---	AAAACAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGCGAGTGCACAGTGACC
ESTC109	35	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC110	23	---	AAGGGACACAGTGTGCTGACAGGTGACACTGAACANAACAGTTTCCCTTTAAATTGTAAAGCGGG CATCG
ESTC113	37	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCAAAATTTACAAAAAGC CTCCA
ESTC117	24	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATACAGCCTCTTT
ESTC119	24	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC122	34	---	GAAAGCCAGTATGTTGTGGCAANATTCGAGAAACACACTGAAGAAA
ESTC123	21	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCAGGCCCATNTTCCATGGGACAGGCTGGCTCAA TGTGGAAGTGG
ESTC128	42	---	AGTCACCATGCCCGCCAGCCTAGNATGAGTTAGTAAGATTGGTTAGCTGGGGAG GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC129	20	---	GCCTGCTCACAAAGGTAGCAAAAAACATAAATCTCAGGAAAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG
ESTC13	46	---	
ESTC130	49	---	

ESTC132	30	GGTAAAGTCTAAATTACTGCCTTAGCAAAACNCTATGTTGTGAGGTTTTCGCTGCA
ESTC137	21	CCAGTTGGCTCTCTCTCANAGTCTCTCCATGTGGCAACA AGGAGCACAGCCTAAGGACATGAAGGTACAGATTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG
ESTC139	45	GAGGAGG CCATTGTGTGCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCTTGCAATGGTTAGAAAGC
ESTC14	20	TTGCCCTGGTG CCTAGGCTCATACAAATAACAGTCTCAATAACAAAAGACGTAATACTATTTTATTCATTTTAAATC
ESTC142	72	AAAGANACCATTCCATTCTCTAACAAACA
ESTC143	29	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	AAATCCATATTTCTTGACATGAGGNGCTTTTTAGCAGCATTTGCGG
ESTC146	20	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG TCITTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGATGCGCTGATGCGCGCTGTGTGAGGCGCCCTG
ESTC148	42	GGGGTGGCTGGGCTGTGTCTGAG
ESTC149	28	TCAGTTCAITTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	GGATTGTAATATTGCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTTCTCAGTGATCTT CCAGGAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTTATCATAATATCAATATT
ESTC150	20	AAACCTGATGTTTAAAGAACCTAATGAGA GAAGCTAAGGCCCAATTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACCTCAGAGCTTAGGA
ESTC151	49	AACACAGCC TTTTTAATGACAACTCAATCTCTACATACAGTNTTGCAGAAATTAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCAITTTACA
ESTC155	37	GCAGCAITTTGTGACAGGAGAGCGCAAAANCTGGCTGCCCTCGGGATGGAGCGGGGGCGCTCA CCACCACCTGCAT
ESTC156	32	ACCAAGCCCTGGGATTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC158	35	AGCTGGCAAGAGACTTCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACCGGTGCTGTTCTGCA GCITTTGAAGG
ESTC159	31	

ESTC16	23	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGATGATCATCCCCACAAGGACAGGTT TTCTAGCATTGCTGGTGCAGTGGGGGCTGAGCTGGGGGCGAGTGGCAGTGTCTACTGGGCGCGTTTG GGACTGGGTTGA
ESTC160	38	CTCTCGTCCGTTTGCAAGTTGCTGTTTTCAGNTACACCAGTCAGAGCTCCACAG TCATTCTCCATAGAATATTGGTTTGTAAACANGAATACAATCCAATATAAACATTAACAATCC GATACATACCA
ESTC162	36	GTCTCTGTTGTCAGGGGAATCANITTTGCTGGATTAGAGGAAGGTGCGCGCTCTGTTTCCATGACTT
ESTC164	31	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA TGGGTGGCTCTTTAAATACCTTCCAATATATTTTCAAAATTTTNCITTTATTTAAATACCTTTTAT TCTCTTATTCCTATATAAAGGCAACCAA
ESTC169	22	TCAGACACTGCCGAGCATCAGCATTGCTCTGNTGTACAGCTCCCTTCCCTGAGGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC176	23	TAGGGATTCCAAGTTGCGCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC177	42	GCTTGACTAGCGAGGCTACATCACAAITTTATAAAGTGCCAGATNAGTGTAAITTTGTCATTCAGCTTG ATTTTCACTCA
ESTC18	29	ACCATGATTGCTCTACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGATGGCTGG TCTATTAAACAGGGTTATGTACACACCTGTCACACCTCAAAACAGATGATCTCATCTACTGCTTCCAT CTTGC
ESTC181	21	AAAGTACAAATCCAGTATATGCAGAAAGNTACTCAGGCATCAGCTCGTGATCA TCCTCAAATACCACTTCCCTAACTTATCAGTCTAGTAAGCNITTTCAAAGGAGGAAAAATGGGTTAC CTTTCAGGGG
ESTC186	43	ATCTCCAGTGTCTGCTGCCCTCCCGNGCAAGTCTCCCAACAGCACA AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACCTCCAAGAACTCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC187	24	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCAATTAACAGTACTTTAAAT CAATTACTCTCTTTTGGCTGCAACAG
ESTC188	25	
ESTC189	27	
ESTC196	42	
ESTC197	26	
ESTC20	33	
ESTC200	44	

ESTC201	35	TCCTACTTGGGTAGTTTAGCAACATTTTAAANNCACATCCACAGATTGGTT CTGCTGGAGGGAGGACAGACGCGNCAGCGCGCTGGGTGGCGGCCGAGAAAGGCTGGCGGTGATGTT CGAGATGAGCC	---	---	---
ESTC202	22	ACACTTAACAGGTTAAATAATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTATTTGTGCTAC AAGACAGTTGCA	---	---	---
ESTC203	27	TATAGCCCATCGCTCTCAGTTATTAGAACTCTGAGAGGGATANAGCAATACTATTGTTTAAAGC CTAAGAGTGAATA	---	---	---
ESTC208	43	GATGAAGTGGCTTCCCTTTGGCGAAAGGATNAGAGTGAGTGACGGTGACCTGTG GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC	---	---	---
ESTC210	29	CTCCAGAGTCCTCTCTCTANACCAGGGGCGAGGGAGGTAGGGAAT TGGGAAGAAATTTATTACACTAACAAATTAATTTAATCAGAGTATTTTAGATTGGTCAGAAAA CAAAAGACCA	---	---	---
ESTC212	27	TTTTGTCAAGTAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAAGTTTCAT AAACACACCCCA	---	---	---
ESTC214	21	GTACACATCTCTGGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGGAAGC	---	---	---
ESTC216	49	TCATTGAAGAAAAATTATGGGTTTTATCTTTATTTCTAATTGNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC	---	---	---
ESTC217	28	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGGAGGGA CGAAGGTAGATTTCCTCCACATATTACAAAAATACACANAACACACACACACACACACA	---	---	---
ESTC219	32	TGCACTGTGTACTCCCGAGACNGAGAGCTTACATACCATATAGAAAGAGCATAGTGCTTCAGAAAGGA ATGTGTAGGATCG	---	---	---
ESTC22	41	TTCTACTTTATTTCATATTCACACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAGGG	---	---	---
ESTC223	27	GGTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA CAAAAGGGTTAGTCATATTCGCCCANCAACAGCATGATAAATAATTC AAC	---	---	---
ESTC224	37		---	---	---
ESTC225	20		---	---	---
ESTC23	27		---	---	---
ESTC230	43		---	---	---
ESTC231	24		---	---	---

ESTC28	23				GAAGAGCTGGGCACGCATCTGACNTTTCCTCTATTCTTATAAAATAAAGGAAGCAGAAATCT CC
ESTC3	20				CAGACATGACCTAACCGTCCCGCCCTCAATTCATTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32				ACAGCCCCACAGAACTATTGTAAACAATAATINTCAGTCGGTGATCATTTGTAATATACATAACAAAG CAATTCCTCAGA
ESTC33	25				AGCACTCCAGCTCCTTGACGTTGNGGACACAGGAACCTCCGGAA
ESTC39	26				AAGGAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCCTGGGCATTA
ESTC4	23				CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTATGCTGATGGAAAGAAACCATTT
ESTC40	22				GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAATAATTTTGACTTGTCCCCCTTCAC
ESTC45	37				TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTAAACNCCTCTCATCATCAGAGGCTATATATTA CTGTCCGTGGTGAGCCCTGCCGCTGTCCATGGGCCAGGAGCCACTGGTGGGANCOCGGCAGATG TTTACCCCTGT
ESTC50	56				GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC56	45				AAAGTGGCCCTCCAGTCCCNCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC57	20				GAACACAAAAGTTGAGAAAAAACTTCTCAAAATTTGCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAAGGC
ESTC59	38				TCTGCAGCAGCTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC6	27				AGTGATTTTGGCTAGGCTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGANCCTCTCTCCC ACCCACTCAAG
ESTC61	57				ACAGACAGCATCACACANAGGGCCACGGAGGGTCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC63	20				GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCACACTTACTTACTGCTCATCCGT CACTTTCGGCTAA
ESTC69	20				AGTTTCCCTAGAGCTGTGGGCCAGATAGTGTTCCTGAGTTGCANGCACGATGGAGATTGGACACT G
ESTC7	45				

[illegible]

DWU-252	94	A G	...	AGTATCAACATTTAAGTGTGTCAGGCTACAGATGCTGACAGGCACCTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCTCAAGTGTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCAATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTGAATGACAAAGTATGTGGTTTGTA AT
DWU-330	85	C T	...	GAACATTCCTCGAGCACCTCACTACCAATGASCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCAATTATGTGGACTGAATCTCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTTTTGCAA CAAGACAAAGCAAGCCACATTTTGATTAAGACAGATGACGGCTGCTCGAAGAACATGTTCAGAAA CTCGATGAATGTGTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A G	...	GAAATGTTAATTGGGAGGTGAAAGGGTACAGATGCTGTAGCAGACCTTTGGTTTAAAGAG AAGCATCATTTCCCAACAGGCGCACTGTAGAAGGCCAGCTGAAGAGTAAGGAAAGGTCTGAGG ACTGACCTGTGGCTGGCTGGAAAGGTGAATGTTAGGGCCCTTCACTTCCATCACAGAAAGTC ATTAGACGGTACCAATTCAAGTGTCTGTTCTTATGAGCATCTATTCTCTGTGC
DWU-1537b	89	A G	...	CTCTTAACCTTCAGTTCCTCATCTATAAGAAATGAGGATTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACAGAAACCCAGGAGCAAGTGGGACCTGATCCACAGTGAAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T	...	CTCTTAACCTTCAGTTCCTCATCTATAAGAAATGAGGATTCAGTTGTGATCACTATAGCTCAGGTA ATCCAGGACCAAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGTAACACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G	...	ACCATCTTACTATGTCAGGTAAGTCCATACAGAAAGGCCCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTGCGJAGA CCGCGACACCACTCTGAGCTTTCTGGGCTCTGAGTCTGTCTC
ESTD-ADAA	184	G A	...	ACCATCTTACTATGTCAGGTAAGTCCATACAGAAAGGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTGAGCACTGAGCTGSCAGA CCGCGACACCACTCTGAGCTTTCTGGGCTCTGAGTCTGTCTC
ESTD-ANT1	160	T C	...	TCTCTGTCTTCTACTCCATTAGTTCAGGTCAGTGAAGCACTGGGGCAATTAACCAAGTAATCA TGCACTGCCCACTGCCAAACAAAGAGGGCGAGTGGAGCAGGAGTATTGCTACGGCGGTACCTT TTTTATGGAGGACCGAAGTGAAGCTGAGCTCTGAGCTCAGATGATCTGT
EST10398-2b	168	A G	...	TGCTGGGTGGCAAGGCTGCAACAGGAGGCAACCCAGGAGCTTTATGAAGCGGCCCATGGTA AGATGCTGCCACCTTATCTACTTGTGATGTTGACATTGGGGCTTGACTTTCCAAACGAGGAAG CATGTTTCTCTGGGCCAAGAGGATATCTACCAAGTATGATAGTGTCTATTAGGCATTG

EST10398					TGCTGGGGTGGCAAGGTGCAACAGAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA
2a	147 C T	AGATGCTGCCACCTCTATCTACTTGTATGATGTTACATTTGGGGCTTGACTTTCCAACACGAGGAAG
ESTD-C7	14 G C	CATTGTTTCTTCTTGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-					ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAACTCCTGTGGA
D4S95	90 T C	CTTTCATGCACGATAGCCTTCTCTACTAATCACAGAAATTTGAGAGAGCAAAACAACATTTCAAGG
ESTD-					ATAATGGGGCAATCACCTTCTTCTTCTCTTTAGAGTCTACCGG
GPPK2L	38 G A	AGTCTCACTCGGGTGTCCAGGTAGATCCCTTTACAC[G/AJCCGAGAACTGCTCGATATC
ESTD-					CTGGCTGCCCCGACGAGCTGCTGGCACCTGGACGGCGGCCAGGCTCAOCTCTATAGTGGGGTGG
HRASb	82 A G	TATTGCTCCACAAA[G/T]GCATCTGGATCAGCT
ESTD-					CTGGCTGCCCCGACGAGCTGCTGGCACCTGGACGGC/GTGGGGCCAGGCTCAOCTCTATAGTGGGG
HRASa	37 C T	TCGTATTGCTCCACAAAATGTCATCTGGATCAGCT
ESTD-					GGAGCAGGAGGTGGGGGGGGTCTGCTCTGCTCCAGGTCCACAGACAGAGAGAGGGCCTCAGTG
NRAMP	81 A G	TATCCCCACCCCA[G/T]GTGGGGCTGGGAGATGAAGAGGATGTGTCAGGT
ESTD-OTC	18 A G	GTGACCTCTCATTAA[G/A]AACTTTACCGGAGAGAAATTAATAATATGCTATGGCTATCAGC
EST38751					AGATCTGAAATTTAGGATAAAACAGAGAGAGGTATGTAACA
7	36 C T	CCAAAGTCGTTCAATTTTAGCTTTGCAGGTTTAACTC/TGATTACTTTTTCTATTCAAATCTCTGTA
					AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
					CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACTTTGTGGCTGAC
					TTTATGGCTAAGAAAGTTTCTACTGGATGCAATTAATAACAAAT[G/T]TTTACCTTTTGAATAATAA
					ATGAAGGATTTGACCTGCTGCTGCTGGAAAGAGTATCCGTACCGTCTGACGTTTGAACAATACA
EST40562	109 A G	GATGCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
					GCCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA
					GATTGACAGGTTTCATGACAGGCTGTGACAGGATGAAGAGTGGCTGCTCCCTGA/C/TGGGAGCCAGT
EST18288					GTGGACAGCACCCCTGGCTTCAACACCTACGTCCTCCACTTCCAGGTAAGGCAACCTCTCTGCTGGCTC
3	121 C T	TGGCCCTAGGACTTAGTATCC
ESTD-AK-					GGGAGTGACAGCTAGACGCAACCAAGGGGGCTC/TJACAGCTGTGTTCTATCGAGGACAGGCTTCT
168	31 C T	GCCTACTCTGG
					AATCCAGCACTTTAGGAGGCTGAGGCGGATATCACAGAGTCAGGAGTTTGAGACCACTCTGA
					CCAACATGTGAACCCCACTCTACTTAAATAACAAATAGCAGGATGGTGGTGCATGCCTGT
					AATCCAGGAGGCTGAGGAGGAGAAATGCTTGAACCTGGAGGGGAGAGGTTGTGGTGGCCGA
ESTD-ALB	180 A G	GATGGCACCATTGCACTCCAGCCTGGGCAACAGAGTAAACCTCTGCTTTC

EST70523 3	182 G T ---			TTCCGCCAGCCGCCCATCTCTGGCAACCTGGTCCCTCAGGGGCCACCCCGGGCACTCACCCCTCT CGCTCTCGGTAAATCCGGCGCGCGCTCTTGAGCACATAGCCTGGACCGTTCTCCGTATAGGAGG ACCGTGTAGGCTTCTCTGTCGGGGCTTGCCAGGGGCCAGCCCTGAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGAGTGTCTCCACGCTG
ESTD- APOA2	101 C T ---			CCAGGTGTGTGGCACGTGCTGTATCCACGCTACTCGGAGACTGAGGCAATGGAATCTTTTGAAC CGGAGGGGGAGGTTGAGTGAGCTGACATCGCTGCGCACTGCCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---			CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATCAATTTGGTTACAGGAGGCTTT AAGTTCAAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCTCTAGAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACATTTGTCACTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACCATGAAGGAGTTGAAGGCCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGTGGCGGAGG AGACCGGGGACGGCTGTCCAAAGAGCTGACAGGGGGGAGGGCCGGCTGGGGGGGAGCATGAGGA CGTGGCGGGCCCTGGTGCAGTACCGGGGAGGTGCAAGGCTGCTCGGCCAGACACCGAGGAGC TGGGGGTGGGGCTCGCTCCCACTGCGCAAGCTGGTAAGCGGCTCTC
EST43211 8	132 C ---			CGCTGTGTGCACTAOCGGGGGAGGTTGCAAGGCCATGCTGGGCCAGGACCGGAGGAGCTGGGGGTGG CCTCGCTCCCACTGCGCAAGCTGGGTAAAGGGCTCTCCGGGATGCCGATGACCTGCAGAACGGCC TGGCAGTGTACAGGG GG
ESTD- ARSB	126 A ---			GGAAAGAAATGGAGCTGTGGGAAGGAGGGCTCCGAGGGGTGGGCTTTGGCAAGCCCTTCTGCA AGCAGAAGGGCGGTGAAGAACCGGGAGCTCATCCACATCTCTGCTGGCTGCCAACACTCATGAAGCT GGCAGGGGACACACCAATGGCAACAGCTCTGGATGGCTTCGACGTGTGGAAACCAACCATCAGTGAA GGAAAGCCATCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTCAATGAGAACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGGCTGGGGCTGACCAAAATATACTGGGTTTCTGTTCTTTCTGATCAT TCTTCAAGTTACTCTTATTGGAAGGCCCTTAAAGAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCACCAAGGCTGCACCATGTTTGAAGTTGAGTGACATGTTTGAAGGCTGT CCATAAGTAAATTTTGAAGAGAGGAGCAAGAACATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGTACTTTTTCAGATTGAAGGAGAAATGTCATTATGAGGCTGAACCCGACTTTTCTTAAAGC TCTGAACAAAGCTTTCTTTCTTTTGAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA
ESTD- BA511	29 A/G ---			GGGCAACATAGTGAACCCCTCTCTACATGAAATACAAATATAGCCAGGTGTGTGAGCAAG TGCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCCAAGATGGTGCCACTGCA

[illegible]

ESTD- CB22	119 C T	GGCAAGTTTATTGATAGAGAGGAAATCAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGACAGACATGGGAGTGCACCCATAGGAGCTGGATACAAAAG ACAGCAAGGAGGGTAGAACATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	138 C	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTC TTCATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAAGACAGCT CTCAGAGAACCTAGCCCAATACCTCTCCCTTCCAGAGGACCTGAAAAGCTGTTCCACCCGA GGTCCGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A	ACAGGACCAGACAGCTCTCAGAGCAACCTAGCCCAATACCTTCCCTTCCAGAGGACCTGAA AAAGTGTTCACCCAGGCTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAAG GCCACATGGTATGCTGGCCACAGGCTTCTACCCCGACACGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTGCAGCACAGACCCGACAGCCCTCAAGGAG
ESTD- CB25	146 A G	GTTTCTTCAGACTGTGGCTTCACTCGGTAAAGTGTCTCTCTTCTCTATCTTTCGCCGTG TCTGCTCGAACCCAGGGCATGGAGATCCAGGACAGAGGGGCTGAGGGGCGCAGAGCCACCTG TGCACAGGTAGCTACATGCTGTCTTGTCAACAGAGCTTACAGCAAGGGTCTCTGTCTGCC ACCATCCTCTATGAGATCTGCTAGGGAAGGCCACCTGTATGCCGTG
ESTD- CB27	125 C T	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTGGCCCTGGTTGCAATTCAGGAGTGTCTGTGGAGTCTGCTCATCAGTCACTGACCTTATCTTC TGATTAGGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCCACCCAAATGCT GCTTCTCTGTTCATCTGATGAGGAGTCTCAACACCCATTTCCATACC
ESTD- D4S338 ESTD- CYP206	59 A T 61 A G	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATGAGCAGGTATATGA/ATATGTA TTCTTAAACAATAAATTTGAAAGTCCAAATTTACTCTTGTATCCATGGAGTGCAGAAATAATGTTA TTTTAGTGTGCAAAAACAATACTAATCTTGATATGTTATCAGAGCCCTTGGTGACCCAGGTGTA TTGCCAATAAGCAGTAATATTTTGAAGGAATCTGTCTTCAATGCAATAG CAGGCCAGGCTGTGAGGTGGTCAACATCCCGCAGAGAACAGGTACGCCACCACTATGAGCA GGTCTCATCAATGAAGTCTCTCAGGGTCCCTTGGCTGAGAGGGCCGAGAGCACTACGCG AAAAAACAATTTAACACCTTTTCAATCATATACACCATACATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCCAATTAAGTCAATCAAAATGTCATTAAGTAAATGCAAGTTCAACAG ACAAGTTCCCAAGCATCTACGATCAGAAAGGTGAAAATATATCTGGAATTAATATGCCCCA TATCTGCATGTC
ESTD- D11S1873 ESTD- D17S33b	40 A C 169 C T	CATCCCAAGCCCACTCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACATCCAGGGGGCCCTACCTTTGTATCCATGGGAAAGGCTCTCTGGGGGGTG GGGTGTGGCTATGGTGGTCTGTGAGAC/TTGGGGCTTTGGTTTCAGTTGCACTATTGCGTT ATTGCAAGATTGCTTTGCTTTCCACTGAGCGAGCCCTC

ESTD- D17S33a	75 C T	CATCCCAAGCCATCCTCTAGCCACTGGCATTTTGGCCCTCTGACAGATACACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGATGCCATGGGAAAGGCTCCTCTGGGGCG GTGGGTTGT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCCTC
ESTD- D18S8	133 A G	TTTGAGACCACCCCTGGCCAAACATGGCGAAATACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCGAGGAGAAATTGCTTGAACCCJA /GJGAGGCGAGAGCTTCAGTGAAGCAAGATCACACCACTGCACCTACAGCCCTGGGTGACACAGTGGAA GACTCTGTCTCAA
ESTD- D3S11	44 G	AACCTGATTAGAACCTGAAATATACATATTTTATCTGAAAAAAGTCGAGTTATTTGGCTCATCACATTGG AATTTTGCATCATTAAATAATCCAAATAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAACTATTATACATTTATTTATTTGTAAGCCATACATAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G	AGGTTCCACATTTGCTGATTTGCTGATTTTCQJAGJGGAGCCCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGCTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAATTCAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGTG TGAGTCTTTATCAAACTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGTATTTCCC AGAAAGTGAACATACCTGCTCTAGAGCCAGAGTCACTGAGATGTTCTGTTTCTGTTTCTGAGTGG CAGGTATGAATATAATAATCTGTCTTTTATTTGGAAGGATGCCGTGCTGT
ESTD- D3S2a	248 G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGTG TGAGTCTTTATCAAACTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGTATTTCCC AGAAAGTGAACATACCTGCTCTAGAGCCAGAGTCACTGAGATGTTCTGTTTCTGTTTCTGAGTGG CAGGTATGAATATAATAATCTGTCTTTTATTTGGAAGGATGCCGTGCTGT
ESTD- D7S399	83 A G	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGJGTCTCTCATCATCTCTTTCACAAACATTTTTCATCCATGGACTCCATAC TAGAATTTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTTCACGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGGAGGGAGACA GAATGCTGATTACCTCTGTGGAGAACCAAGACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAAAG ACCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMb	66 C G	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTTCACGTGTGGCTCAAGCAGCTGCTGGGCTCCACT GJTTCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGGAGGGAGA CAGAAATGCTGATTATCTGTGGAGAACCAAGACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAAAG CCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T	---	---	---	TCCCAGCCCTATCGGTCTATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACTCCATCAC ACAAACGGTCAGCACCCCACTGAACCTGCAGATGAATCTGCCACATGCTCATCTCCAAAAGCT AGAGAGATTGCTCTGGGCTTTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C	---	---	---	TCTCCCTTTGGTGCAGAGGCTGCCCGGAGGCCAGGAGCTGGAGATGGAGTGGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCACACACAGCTGACTCTCCCGGACCCG TCCCACACGGTCTCCACAGCACTCCGACACGCCGCCCAACACAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T	---	---	---	AAGAGATGGCCAGGATGAGCGCCAGTAGGAGAGGCGCATAGTAGGCATGTGGCGGGCCCTGGCTGG CACCTGTGGATTCTCTGCCACAGGTGTAGTTACAGTGGCTGTACTAGCTGGCTCAGAGATGCC ATAGCCAGAGGAGGTGCGTATGCCAAGGGCTTCTGTGAGAGA
ESTD- ERB2	93 C T	---	---	---	TCTTTCAGGATCGCATCTCGCCTGGTTGGGATCGCTCCCTAGGTGTCAGCGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTGCAGTGCCTGGGGCGGGTGCAGACCCACCGCGGGCTGGGAGACTTCA CCCCGCTCACTCCGTTTCTCGCAGCATCTCCGCTCTGTTG
ESTD- ETS2	43 A G	---	---	---	ACTCACAGTCTTTAAGTGAATGTGCGAGAAAGAGGACCAAGGAGCCGCTCTGGCGCTG GCAGTCCGTGGACGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTGCTGGACACA CACAGACTATTTTATAGATTTCTTTTGGCTTTTGCAACAGGACCAATGCAAAACTCTTTGAG AGGGTAGGAGGTGGGAGGAAACACCACTGTCATTTCAGAAAGTTAGTTG
ESTD-F9	111 A G	---	---	---	AGATCCTGATGATTTTCTCTATTTTCTTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCAATTTGAGTTAATATTTGTGAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCC ATAGGTATGCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A	---	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAG GAAGCTTGCAGCTCATGACAAATTTGAAGCTGACAAATACACAAAGAGAAATAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTTGAAGTTGTTTTGAACCTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACCTCAGGTAAGAT
ESTD- GCH	200 C G	---	---	---	CCGACACCGGTGAGTGGGGTGGGAGTGGAGGAGGAGGAGGAACTGGGGTTTAGGGACT TTCCGGGTGACTTTCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGACACAGAGCCAACTGGCTAA GTGTAAGGGAGCTGTGTCGACCCGTGTCTGCTGCCCTGTCAGCTGCTGTCTGTGCCGAGTTC GAGCTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCX	88 A G	---	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACGCCCTGTCAGGCCACTCTCTGGTCAACATGAC AACCACAGGCCCTCTAGGAGAGACAGTAAAGCCCTGGCAGAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGGGGCTGAGCCGCCAGGAGAGGAGGCTAGGATGTGAGAGACACAGTIC ACCTGCAGCCCTAATTACTCAAAGCTGTCCCGAGGTACAG

EST34088	62 A T	---	GTGGGGCAACAGTGGGAGAGAAGGGCCAGGGTATAAAGGGGGCCCAAGAGACCGGCTC(AT)
ESTD-2	---	---	ACAGGTAAG
ESTD-GNAT2	56 A G	---	GACCCGTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACAC(A)GGCATCA
---	---	---	TTGAACCAAGTTTCCGTCAMAGACTTGAATTTACGGTAAGTGCATGGTTCCTCCTAGG
---	---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG
---	---	---	CAGGAGAGGAAGATGTGTACAGTTTGTGACAGAGAATAAAAGGATAACCTGGGGTTTTCTGTGC
---	---	---	TTGCTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGACGGTATACAGGGACAGCA
---	---	---	AAGCGAGTGGTGAAGTTTTCAAACAAGACACACCTT
ESTD-HT2	154 G	---	AACACAAAGCCACGAGAAATTGAACCTCGGACCCCTGGTTTCAACAGCACAGTCTCTAACCCCT
---	---	---	GAGCTATGGAGCCCTGCTGCTGTTTTCCTTTTCATCTTATAGATTGATGTTATGCTCCTCA
---	---	---	GCATTCGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATCTCTACAAAATGAAA
ESTD-HT5	149 C	---	ACATTTCTGCTCTGTAATCCCTCGAAAAGGTTCT
---	---	---	CTGAGAAACAATTTGGCAAAATAAGGAATTTTGGCACTCCCAACCCCTCTTTCTCTCCCTTGGA
EST37382	124 A G	---	CTTTGAGTCAAAATTTGGCTGGACTTGAGTCCCTGAACCAAGAGAAAAGG(A)GCCCCAGA
ESTD-5	---	---	AATCACAGTGGGCAAGCTCGGCTTACCGGCTCTCCCTCTCACGGGAATTTTCAGGGTAAACT
ESTD-IGFBP1	43 C T	---	ATCCAGTGGAGCCGCTCATTCGACGGTCTTTGGCAGGAGTG(C)CTGGGAGAGAAGGAAGATG
---	---	---	TTCCAGGGCAACATAGCTTAGTGGAGACTC
---	---	---	TTTACTATTTCAATGGATACAGAAATTTGGGAGTCACTATATCTTATGAACAAAAATTCAGATTT
---	---	---	CAGTGTTAAGTAATGTTGCCATCATGTTGAGTGACGGGCGATGTGGTGAGTCCAGAGTGTGGTGG
---	---	---	TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT
ESTD-IGHV4-6	120 C	---	ATGTAAATCTTCACAAATCTAATAAACGGAGTTGAATATAAAACCCA
---	---	---	CAAAAGTAAAGCAACCAATAATGTTAGCTATTACTATCATTTATTTATTTATTTATTTTITG
---	---	---	AGATGGAGCTGGCTCTGTACCCAGCTGGAGTGCACTGGGAGGAGCAATCTCGGCTCACTGCAAGCT
---	---	---	CTGCCTCTGGGTTTACGCATCTCTGCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC
---	---	---	ACTGTTCCCGGCTAATTTTGTATTTTGTAGAGACGGAGTTTCAACGTT
ESTD-IL1A	110 A G	---	CCACTTACAGATGGATAATGGGTACAAATGAAGGCCCAATAGCCCTCCCTGTGTATTGAGGGTGT
---	---	---	GGGTCTCTACCTTGGGTGCTGTCTGTGCTCTGAGGGAGCTCTCTGTCTCAATTCAGG
ESTD-IL1B	99 A G	---	TTCCAGGTGGCTGACCCAGCCCGCCAGCTCTGCAGAGGGAGAGCTGCTGGCTGGCTCGTAAGCATG
---	---	---	TCCGGGTGAGCCAGCCGCCCAAGCGACGCACTGGCCCTTCAGCCCTTCAGCCCTGCTGCTGTGTAT
---	---	---	TTCCAGATACCTGCTCTTCTGCCATGGCCCTGTGGATGGCCCTGCTGGCCCTGCTGGCCCTGCTGGCC
EST374082	124 A T	---	CTCTGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGTGG

EST45311	0	151 C T	---	---	GGCCCTCTCTCTCCAAATCTGTCCTATAGTTTCTCTATTAAGTGAACATACATGCAATCTTTAGT GGATAGATGCACACAAACACAGCCATTATGGGGAAGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCTACCTCTTTTAAACAGCCCTTATCAATGGCCCTTTTCTTTTCAGTA GTACATACACATCTGTCTTTGTTGAT
EST65258	8	80 A G	---	---	TGCCCATCAGCGGCCGAGACATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAAACCAAAAT CCAGTTATTTCCAGJCCCTCAAAATGACAGCCATGGCCGCCGGCTCTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGACAGCTCTTGCAATGGAGCTTGAGGAGGGGCTTGAGGTTGGT CAGGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216	3	26 A T	---	---	ATGCAGGATGAAGGTGGACAGGGAGGATGAGGGCCCAACCTGTCATCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149 G T	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACATAAATATTAGCATTTGTTTGGCATTACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTCTCTCTGTAAGTGCAGATATCCAGAGTTTGGTTTGTGAACATGCAATGCCTGTGAA AAGAACTGAATACCTAAGATTCTCTCTGGGGTTTGGTGCATGCA
ESTD- KRT10b	183 C T	---	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAGGAAGAAAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT10a	133 A G	---	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAGGAAGAAAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8b	231 C T	---	---	---	ACCCCTACCCCTCCCTTAGCCGCTGGGAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGGCTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCCGCTCAGGTTTACCACTGTGTCACATTTGACACA
ESTD- KRT8a	21 C T	---	---	---	ACCCCTACCCCTCCCTTAGCCGCTGGGAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTCTAGAG TTTGTAGAGGTCAAGGGCTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCTATCTCTCCCGCTCAGGTTTACCACTGTGTCACATTTGACACA
EST75099	6	82 C T	---	---	CACCTGTGTGTAGATCTCTCAGTGGCCGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAAGCTGGGGCAACCGGAAGACCATTTGGAGGATGAAAGAGGCTGGCCACC CCTCTCTCTGGCCGCTCTTGAAGGTGTGG

ESTD-PAR	120 A	CTCTCAGGAACCAACAGTCTCTACCAACACGACATATTGCTGTCGAGAGGTACAAACCGTAGA
ESTD- Per/RDS	74 A	G	...	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGCTCTGAAGACATGGAGATACGCT
EST68308	29 C	T	...	AATCGACTGGCTTCATTAGCTCTGTGAGTGTCTTCTTCTTCTGCTGTCTAGAACGTTTCTTAG
EST54045	39 A	G	...	GACTGGCAGTTTAAGCTTTCACTTAGCTTTCTGTATACCATGCC
EST76136	39 C	T	...	ACCTACAGACGTGCTGGATGGTGTGTCACACCGAGGAATCTGAGACGAGACGAGGCTGGCTG
ESTD- PXMP1	88 A	G	...	CTGGAGAGAGAGCTGCGGGAGACCTGGAGGGCT
ESTD-RDS	127 A	GGAAAGAGATTAAAGAGCTTGATTTGGAC/TJAATCTGTTCTTTGAGTGTGGAAGAGTTTATGTC
ESTD- s14544	94 G	T	...	TCTGCTGAGTTACACAGAAATCCTTTTAGTACAGCGAGTAAATAGATATATTCGACACAGATGGGAAT
EST52908	45 A	C	...	GGAGAAAGTAGACTTTAAAGGTAAAGAGTAGTATTTT
EST19590	55 C	T	...	GGAATATTAATAATATTTAAATACCTCCATTTTGTG/TJAGTCTTTTGTGAAGATGATACCTGC
EST76136	39 C	T	...	AAAGACATGGCTAAAGTTATGATTTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
ESTD- SPTB	176 C	T	...	TCTGTTAAGTAAGTACTGTTTGGCTTGGAAITGGATTTTAAITGACTTTATCAT
ESTD- s14544	94 G	T	...	ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTA
EST52908	45 A	C	...	ATGCAGAAAAGAGGGGAAAAGAGAGAGAGCTGTGGTGGACAAAGGTGTTTCTCAAGGCTCATAC
EST19590	55 C	T	...	AGATTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAGTCTTATGAAATTTATAICTT
EST76136	39 C	T	...	CCCGAGGAATCTGAGACGAGCGAGGGCTGGCTGCTGGAGAGAGCGCTGCGGAGAGACCTGGAAGG
ESTD-RDS	127 A	CTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCCGAGGCGCCAGACGACAGG
ESTD- s14544	94 G	T	...	CCAGGCCCCAGAGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAAACACTGAGAAATAGTGCCT
EST52908	45 A	C	...	CCAAGAAACGTGGATCTCCCTCATCCACTCCGAAAGTCTGAA
EST19590	55 C	T	...	TTGGGAAGTTAGAGCTATATTAATTAAGGAATTAAGGCAATTAAGGACGACACAGAGGCTTAATTGAAA
EST76136	39 C	T	...	TATCCCAAAGTTGAAATGTCTCAGTTC/GTCTGTGTGGTTAGATGCAAGGATTTATATGATCCGTTA
ESTD- SPTB	176 C	T	...	ACCTCT
ESTD- s14544	94 G	T	...	ATCACAGGTCTGTGGTCTCTGGCCATCATTTCTCTGGGAGAGATG/GTGGTGGTCTGCAAGCCCTT
EST52908	45 A	C	...	TGGCAATGTGAGATTGATG
EST19590	55 C	T	...	AGGAGAAGCTGAGGAGGGGAGAGAGACAGAATGACATTGATGATGAAGATGTC/TJGGCTCAG
EST76136	39 C	T	...	GATGCCGGGAAATGAC
ESTD- SPTB	176 C	T	...	TGAAGCTTCTGCCACCTTGCCATTTGTTCTAGGAGAACCTGCTGGTCTATACCCTTATCTATAGCCTT
ESTD- s14544	94 G	T	...	CCCTAGGCTCT
EST52908	45 A	C	...	TGAACACCCCTGTGGTCCGAGCCAGGTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG
EST19590	55 C	T	...	CAGTCCCGCCGACCTGTGCTGGTGTGAGCTGGACATACACCTTCACTCTTTGGCCCGGAGAGAC
EST76136	39 C	T	...	ATTACCCACCTGGCCATGTCCCTGGCTGTGTGTCAC/TJCCCTCTGTGAAGACCCCAACCCCTGC
ESTD- SPTB	176 C	T	...	CTCCCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-1AT	224	C	AAATGGTGAAGACCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGATGCTAAGTCAGCACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAAOGTTTGTTCACACTTTCTCCAGTATGGATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THB	125	A	C	TGCGGCTTTCTCGGCGAGGGTAGACTTCTACTGGCTGTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCAGAGGATC/CJCTTCAT CCACACTGGATTGCCCCAAACAGTCTGAGTGCAGCCAGGACTCAACGGTCCCGCTGTAGATGGG TAGTGAAGTTTTCATCTCTCTGAGCTTCTGGATTCTTTGCCACCGCAACAGAGAGTCTATGC CAAGGCAAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCAGTATCCGCCAA GCAGTGCATCCATGACACATAATATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTGATCCATTTTCATTTGGCCATAGTCCCTATGGGATGACA
ESTD-TYR	122	G	T	AGTAGTGATGAAGCTAACAGCCCTCTCCTCACTGATCATCAATGCTATGCTGAAGAAATGAA AAACTCCAGAATCCTAATCAGTCTGTGGCTAACAAATGCCCTACTCTCTATGCAATTAGTATCACA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACITTTATTACCTTTCTCT AATACAAGCATATGTTAG/CJATTAAAGTTCTAGGCATACCTT
ESTD- TYRP1	222	A	C	AGTAGTGATGAAGCTAACAGCCCTCTCCTCACTGATCATCAATGCTATGCTGAAGAAATGAA AAACTCCAGAATCCTAATCAGTCTGTGGCTAACAAATGCCCTACTCTCTATGCAATTAGTATCACA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACITTTATTACCTTTCTCT AATACAAGCATATGTTAG/CJATTAAAGTTCTAGGCATACCTT
ESTD- TYRP1	222	A	C	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAGGTCACAGACAGGAAACACCCAGTG ACTCTGAGATGTCAC/CJTCAGACTGAGAACCCCGTTATGTACTGTTATCGACAAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148	C	T	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAGGTCACAGACAGGAAACACCCAGTG ACTCTGAGATGTCAC/CJTCAGACTGAGAACCCCGTTATGTACTGTTATCGACAAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148	C	T	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAGGTCACAGACAGGAAACACCCAGTG GTGACTCTGAGATGTCACAGACTGAGAACCCCGTTATGTACTGTTATCGACAAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74	A	G	ATGGGCTGAGGCTGATCCATTACTCATAT

ESTD- SSA1	111 C T	...	TTACATTTGGGATGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCGAAG TTTGGCTTGGCTGCCCTGTGCTTTGGGATAATTTGAAGAGATCTTTTGGCCAGTCCCAATGTCCTAGA GAGTTTCCCAATGTTTCTTGTAATAGTTTCATAGTTTGAGGCTTAGATTTAAGTCTTTAATCAATT TTGATTGATTCTGTA
ESTD- RVR1	109 A G	...	CTTCGTGACGGGAGGTACGTCTCCGCCCTCTTTCATGGACATATGATGAGTGTGACCATTTCCC CTGCTGACAGTGTGATGACAGCGGAGACTTGTCTACTATGAGTGGGAGCTGTGTGCATCTATGCC CGCTCCCTGTGAGGCTGGAGCCACTGAGATCAGCTGAGTGGGAGCCAACTTGGCTGGGGCCAGCC ACTCCAGTCCGGCATGTCTACTACCGGCGAGTACCTAGCGTCAACCGAGG
ESTD-WT1	70 A G	...	AAGACCTACGTGAATGTTCAATGTGCTTAAAGCCCTCCCTCTTCTCTCTCTCTGCTGCGATGTG CGTGTGCTGCTGGAGTAGCCCGGACTCTTGTACGGTGGCATCTGAGACCACTGAGAAAGGCC CTTCATGTGTGCTTACCCAGGCTGCA
ESTD-F2 EST44438 7	100 C	...	GATAAGTACACTGAGGCGCCAGGAGGTTATTGCCGTAGTACCCAACTGTGCATGCAAGCTTAACTCT GCACCAATGGCTCCAAAGCCCGTAGGGGAAGTCTAGGGGATCTAGGGGATGGGTGAGGAATGGCC AGCCAGTCCGGCGCGGTGCTGGTCCCAACAGAGAGGCGCGTGGAGGAGGACAGAGGATGGGC TGGATGAG
ESTD- PBDA	103 A G	...	GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJS TCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G	...	CCTTCTCATGCCCGAGATGGAATTCAGTCCCTTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GTCTTACCCGAGCTTGTCTGCGCATACAG ACGACAGTGTGGTGGCAACATTGAAAGCCCTGTAAC
ESTD- CTLA-4	48 A G	...	TGCAAAACACACAAATCTTCCAGATGCCCTATGGCTGTGGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGTGTCAAGTCCA AGGCCATTGGCTATCTCAACACTGTGTGAGTGTATCTTGAAGGAACTTGAATGTTATTCAC TGGATTCCAGTAGTTTCAGTTACTTATGAATATTATGATACATTAGCTTAG
ESTD-ACE EST54419 8	96 C T	...	ATGGCTGCCCTTGGATTTCAGGGCACAAGCTCAGCTGAACCTGGCTTGGTCCAGGACCTGGCCCTG CACTCTCCTGTTTCTTCTTCTCATCCCTGTCTCTGCAAGAAATGCAAGTGGCCAGCCCTGCTGT GGTACTGGCCAGCAGCGGAGCATCGCCAGCTTGTGTGAGTGTGCTTCCAGCAAGCCAC GATCAAGAGTGCACACGGGTCAAGATGGACAGCTTCCACAGTGCACCATGAGATGAGTGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TGTCTCCCTGGTGGGGGGCCAAACCCGGCTTCCA TGAGGCCATTGGGGAGCTGTGGGCTCTGGCTCTCCACTCTGAAATCTGCACAAATTCGGCTTGC CTCTGGCTTAATTTGAATGATATTGTGCTGTGGGACCTGAGCACTTTTATGGCACAATGATCACTA TTTCTTGACCCCTACTAC/GATCTCTGGGAGATGTTTGGGTTTAGCGTGGTGTGTTGTGCTA CTATAGTCCAAAGTGAA

ESTD-PS-1	99 A G ...	---	GGGAGTAAACTGGATTGGAGATTTCATTTCACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAAACACCAACCATAGCTAGTTCGTAGCCATAATTAATGGTTGTGCTTAC ATTATCTCCTTGCATTTCAAGAAAGCATTGCCAGCTCTCCCAATCTCCATCACTTGGCTTGT TTCTACTTGGCCACAGATTATCTTGT
ESTD- B3AR	104 C T ...	---	GGCTGCCAGGGTTCCGTGGAGGCGCCCTAGCGGGGCGCTGCTGGGCTGGCGCAAC GTGGAGGCAACCTGCTGGTCACTGGCCATGCGC/C/TGGACTCCGAGACTCCAGACCATGACCAA CGTTCGTGACTTCGCTGGCGCCAGCCGACCTGGTGTGGGACTCCTGGTGGTGGCGCGGGGCCA CCTGGCGC
WI-567b	48 A G ...	---	TCTCACACTGACCCCTTACCTTCATCTCCTCCTGCTGCCTGGTTCTGAGGCCCTCATCTCTTTTA CAGGATCCGGCCACAGCATCCCACTGATCTGGCTTAGGCTCTCTCTCCAACTCCATCTTCAAAG GCTGCCACTGTGATCTTCCAAAGGTGATTCTGATGCTACCATCTTGTTCAGCC ATGGAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTCCACATCCCTTCTGTGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTAGTTACTATGGGCACATATACGCTCATGTTTGTCTCAGCCACAGAGATTAA CATTTCTGCCACCCCTC
WI-801c	58 G T ...	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCCACATCCCTTCTGTGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTAGTTACTATGGGCACATATACGCTCATGTTTGTCTCAGCCACAGAGATTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ...	---	GAAATCACCTATACAAGAACTATTTCTCTAATTATTTACATTAGTCTCATTTCTGAAATATTAT TTTTACAGAGTACCTTTTGTATTTTGTATTTTGTACGAGAGATTACAAATCAGTAACGC TGTTCAATTGATGCTATCACAATGTCTAAATACCTTTTGGTCAACATCAAAATTAGAAGAAA CTTACAAAGTTTATTGCTTTATGGTTA
WI-1099b	76 A G ...	---	AGGAATGGCTGACTCTCTGGTGGCTTCTATTAGTAAAGGAGATGTAATTGCTGATGAGCCTCT CAATCTCTTAACTGCTGCTTCAGTCACTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTGTAAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGATGACAAGTA
WI-2529	71 C T ...	---	TAAGGCTGCTTCCGCCAGAGGCCCGGAGAGAGAGATCTTGATCCAGGGCCACAAA TGAGCAATCCATACATACATATAAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATTTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGACTTTTACATTTTAGAC AGGTC/GTAGCAGAGCAGCAAGAGGAGAGAAAGGAAAGT
WI-10088	205 C G ...	---	

WI-2625	98	G A	---	---	---	GGCAGTCTCGGCTAGTGGTAGACAGCACTGAAGGATGGAGGAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAAACAAGGCTATTAGGA/GA/CAAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCCA GCCAGCAAG
WI-2924	54	G A	---	---	---	TCTGTTGTCAATTTCCCTCTTTGACTCTGACCTTCTCTATAGG/GA/JACCTGTGATT ACACTTAGGGCTACTGGATTATTAGACAATC
WI-2939	72	G T	---	---	---	CCATTGTGAGGTTGGTGGGCTACTTGTCAATTCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGC CTTTG/JCAAGACCTTCCCTCAACAAGAAATCTTCCATGCCGTGTTCTTTGAAAAATTCGACT TTATCTGAAAAACTCAGCTGCACTGATGTTATCTCGGGTATAAGCCACTCTCTG
WI-3203	99	G A	---	---	---	CTTGCTACCATGCAATTTACAGCATACACCTCAGTGAATCCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAG/GA/JCCACACAGGCAATACTTGAAGTGAATTGGA GAATAAGATTGATGGATGAAGAGAGAGAGAGAGATGCTAAAGTGA
WI-3473	101	A G	---	---	---	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATGGAGATAGTTGGTGATAGCCCTGTTTGA GATTGCAGAGAAGGAAGCAATTTAGCCCTAGGGA/GG/JTAGAAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA/JG/JGACAGGCGTCTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCG
WI-1796b	29	A G	---	---	---	ACACACTTTTCTGTATGCTCTTCATCAAA/JG/JGACAGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCG
WI-1796	29	A G	---	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAGAAAGATGGGGTGAGT AGTCACATTAGGTAATTTCCAAATAA/C/J/AAAAATGCCCTCGAAAAATATCTCTCCCATGTCCCTGTC TAATATAACATTTTCCC
WI-4360	93	C T	---	---	---	GCTGAGCTTTGTGGCAGAGCCAGGCAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAG CAGGAACCAAAATCAGTCTCTGGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87	C T	---	---	---	GTTGTGCTGTAGCAGACACAGAGAGCA/JG/JAGAGAGAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28	A G	---	---	---	CTTGAGTATCGGTGGATTGGTATACAGAAAATGGGAGAGCTGGAACTAATCCCCCATATACCA AGGGACAATTTGATCTGTTTCTACAAATTATACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAACTGACAGAGTTTAAATTGAGTGAATACCATAAAAAATAATATAGTAGCAGCTAATATT TACTGAGCTGTACTAGGTGGCTATAAATAGG
WI-1980b	140	C T	---	---	---	

WI-2015b	190 A G ---				... TGTCAGATAGTCGCTCTACCTAGGTGCAGTAGCATGTAGGAGCTATTAAAGTACACAATTATGCT ATATATTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAAGCCACCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGTATAAACTCTACATGGTGCTTTTCCAACTAG/GCATATACCT CTAATACCATAGAG
WI-754b	49 C T ---				... GAAGGCACAGGGAGAAGATGGCTCATCTACCAGCCAGGAGAGAGC/CCTACATTTATTGGTAA TCCTATAAAGTGCAATCTTTTAAAAATTTGTATTACTTTAGA
WI-754	22 T C ---				... GAAGGCACAGGGAGAAGATGGCTCATCTACCAGCCAGGAGAGAGC/CCTACATTTATTGGTAA TCCTATAAAGTGCAATCTTTTAAAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---				... AGGCAATCAGACCTCTACAGAGGAACCCCAATAAAACTCTGATGATCGTACATCC/GJTGCGCTG GAGGGTGATGCTCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G ---				... AGGCAATCAGACCTCTACAGAGGAACCCCAATAAAACTCTGATGATCGTACATCC/GJTGCGCTG GAGGGTGATGCTCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G ---				... TAAATTTAAATGGGGCCAAATACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GAAGT/GJTGCTTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---				... TAAATTTAAATGGGGCCAAATACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GAAT/GTATCTTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---				... GAGCTTTCTTAAATTAAGGATTGTGACTAGCAACCTCCTGTACAGATTTCCTGTACACACATGTGCA AGCAGCAGCAAAATTTGCCAGCTGOC
WIR-5g	209 C ---				... CGGACAGAGACACAGAGAGAGTTCGACGATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCTGTGGTCCCACTGTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACAACAGG TTTTACGTCACG
WIR-5f	196 C ---				... CGGACAGAGACACAGAGAGAGTTCGACGATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCTGTGGTCCCACTGTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACAACAGG TTTTACGTCACG
WIR-5e	194 C ---				... CGGACAGAGACACAGAGAGAGTTCGACGATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCTGTGGTCCCACTGTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACAACAGG TTTTACGTCACG

WIR-5d	191 A	---	---	CGGACACAGACAGACAGAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCAG
WIR-5c	177 C	---	---	CGGACACAGACAGACAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCAG
WIR-5b	159 A	---	---	CGGACACAGACAGACAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCAG
WIR-5a	37 A G	---	---	CGGACACAGACAGACAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACAC AGGTTTACGTCAG
WIR-6	63 A C	---	---	TAACCCGAAACTTTGCTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AGC] CGCAGTCTGGGGTTGGGCGAG
WIR-7	12 C T	---	---	TTCTGACTATTTC/TAAGCATCTGTAGAATATTGAATACATAGICTTGAGATTGATC
WIR-8	46 C T	---	---	GGCGTCTATGACTATCTCTGGTCACTTGAATTAATGATCTGCTGCTGGCCTTG
WIR-2	56 C G	---	---	AAACAGAAAATAGAGGTTAAGGATGGAACCTAAAGTTGTCAGAGAGGATGA/C/GCTGAAG AAAGAACTACTCTCTTTGACCAATAAATACTAATTTGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G A	---	---	TGTCCTTGCTATGCTGCTCTTTCCGTTGGCAGGATGATGCTGCTATTGTTTACACAAAGTA GCTTCAGAGGGTAACACAGAGTTGATCAGATCTATCTGTCAATCCCAACGTTTACATAAAA TAAGAGATCTTTAGTGCACCCAGTGAATAGCAGATCTTTAACACAGCCGTGTGTTCAAAAT GTACAGTGGTCTTTTTCAGAGTTGGACTTCTAGACTCAGCTGTTCTCAGTCTC
WI-18694	41 A T	---	---	GGTCACTTCTTTTATCTGTACAGGCGCAGCTCTGACTTATCTCTCTGTTCTGCTATCTCTCC CCACATACCAACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A G TGC	CCATATTTC A AGTTTGGAAA	TTGATTGCTG CTTGCAAT	CACACTGTTACACCTATATTTCAAGTTTGGAAATGCA/GJATTTGCAAGCAGCAATACAAAAGTA TTTATGAAGAAATGCAATAATCTCTGAAATATGAAACATCCCT

WI-18517	87	C T	CAGGAATCAG GTGCAACA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCTCAACACCCCTCCTCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGAGCTGTGTGACCTGTGCCAAACACACTGACTGC
WI-18568	76	C T	GGCGAAAAC TAGGCAAAA GCTGTCACTCT AGCATCTGGA	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAACTTTTATTTTCAACTTAGGTAAAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA[CT]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75	T C A	AGCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACAGTACTGTACAGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCTACTCTAGC ATCTGGAAT[CT]GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGGTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGCTGTACCCAGGCTTTCTGTGGGACACACACCAAGGCGAGTTGGCTTGAAGAGGC CTTGAGGAACACGGGTTCTCCGAGGGGTAC[AC]CCAGCAGGGCTTACAGCTTAAAGTCG TGTTGGCAACCTTTGTTTAAATGCAACAC[AG]ACTTAAATTTACAGCACATTCATTAATGAACCAAC AGGAGATTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAACGCAATACAAAGGAAG
WI-18673	29	A G	ACCAGTATGTTTATTTGGAGGTTAATCTCTATTAGGATATGAAGGATTTCAGCAACGATTGAGATT GTGTCTCTACGGAGGGCTCGGGCCAAAGTCTGTGGGTGGGGGTGCAGAGTC[CT]GTGTCTCTTC AGTGTATTTCGGGACC
WI-18640	121	T C	GTCTGGGTG GGG	GCAATACCA TGAAGAGGAC A	TATATTTCATTTTTCATCTAA[CT]TACTGAAGCAATTTCTTTGGTTAACTTTAGA GGGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTAACTCCCGAGATTTCCTTTTATT TTTATATTTCATTTTCATCTAAATTTACTGAAGCAATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTCTATCTGATA CTTGTTCAGATAGGCTACAACCT ATT
D11734	83	A C	TTT	ATT	CCCTGTTCAAGATTCTCA[AA]AATAGTTGTAGCCCTTATCTCTGGTTTACAGATGTGAACTTT CAGGACTTGTGTGACGCTGCAGACACAGACAGCTCATGGGCAACATCATCTGGGCCCCAGAGAG AGCTGCCCGCAGTGCATCATAGGGGGTCTTTCTAGTGTAGTCCCTTAAATGCCAGCTG AGTACCTGAAGGAATCTGGGAAT[TA]TGGCCCTGGCTGAAAGTGGCCCATCATCATACCCACTGTT CT
D49493	159	A T	CCTGAAGGA TCTGGGAAT	ACTTTCAGGCC AGGC	TATTCATAGAGGAGACCTAGGAGGAGTTTACACAGCACACTGCTCAGCAGATGACTTAAAAATTT CCCTTAGCCATTTTGTCTCAAGTCCCT[CT]CTCATCCATACCACCACCTGCTGATTG
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCG	GCAGTGGTGT ATGGATGA	TATTTGGCTACTTGGAGCTG[GA]AAGCTTAAGATTGAGGTTCCACATCTGTGAGGGCTTC CTGTTGAGTTCATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGGGGCTACAGAGCAAGGAA A
EST10052 2	24	G A	GAGGCTG	TC	CTGTTGAGTTCATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGGGGCTACAGAGCAAGGAA

EST12502 2	52 C G	ATACTAGGAGAGAAACCAACTGGAGGCAAGTCCACAGGTACACATTTGCA/C/G/CAGCAAGTAT AACAAAGTGGTTTCGATGAAGAGAGAAATGCTACGGGGAAATGAACCATTTTAAAGGGCCATGTG GTCTCGAGGCGATTAGAG
EST12619 8	105 T C	CCAGAGAGAAATTAGAATGTATCGGTAAAGAAATAGGAATGCAATTTCAACTCACTGTACACAAA CAGGTGTTTATATCCCAATGACAGTGTTCCTGAGAT/C/GATGCAATGTGGCAGACGAG TTTCTCTCTCTCTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTTGCCACCGGCA /G/TTGAGAAACAATATGAAAGAGAGTCACTGCCCTCTGGAAATATCAGAGTATTTGA
EST12620 0	67 A G	TTGGGTTCTCCAGGATTCCAGT/C/ACTCGTAGCTGATGTCATGAGGTCTCATCATGCTCCACGG GTCTGGGAGTGACCGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCACTGGG TCTCAGCTTCCACTGACCTGCAT/C/CAACAGCCAGTTATTTACCAGAAATTTGTTGGGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACTTGTTTG
EST12817 9a	22 C A	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTTAAAAACAACACAGTCTGTCACTTG CAGACCCACAGGACACACATTTCTCTCTCATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST12941 8	23 T A	ATTTTGTGTTTCTAAATGAAGCATAATAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAACCTCCCTAAATCAGTCTCTAGGGCCACA/C/TTGGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAAT
EST12949 2a	52 A G ATACTGTT	TGCTGTCTGCATCAGTCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCACTA /G/ATTTAAAGTTTACAAATTTGAGAAGCTGACACGTGTCTCATACAGACACCTCATTTTACTGTGC TTTACTG
EST13067 4	104 C T	TCTGCTTTTAAAGATCTTCATAGCTGCTTAGGTTTGTTCTTCQ/C/TAGCATATTTCACTATAATCA CCTACATCCCTCCACAAATATTTCTGTGTGGCCAGGCGAGTCTCCTCACTGTCCTCCATGATAGCC AGTCTTATTTCCACTCT
EST13121 6	44 C T	AACCTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATGAAATAGTCT GGCCATTT/G/GACTAACCAAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAACATG
EST13226 6	74 T G	GCATCATCAGGCGCTTTTACTGAACCTTTACACCAACTTCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/ATCTCTGTACAGGAGCGGTACTGCTTCAATCTTTGCATGTCAGGTGTTTACACAGGCA AACAGTTTACTCCACAT
EST13230 6	72 G A AGAGAGC	AAAGATATAAAACAACCTCCATCAGTAGCAATACAAAGTTATACATTTTAAACAGATTTTCTCAGG CCTT/C/TTTGGATACCTTTAGTAGTAACTCTCTTTTGCAACCCCTCTTGATATAACCA
EST13236 9a	70 T C TCTCAGGCT	

EST13278 2a	51	A G G	CTTCCACCGAA CAATAATTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAGAAGCTTTTACAAGCTCCAAACCTTTCACCGAACAAATATTTTAGGAGJATTTGAATATAT TTCTGTAGTTCTCACCACCCCAAGAAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTC AGTCCAAGA	GATGGAAAATT TGAGGAAAGGTT	GCTCAGTAGAGCAATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTCTGAAATTTACTAGCC TGCTCTGAGAATCCACACATTTTCAGTCCAAAGAJTAACTTCTCTCAAATTTTCCATCTCCCATCAGA
EST13290 9			CAATTTTAGA AGTTGGGTT	AAATCAGTTCA TGGAAAATTTCA	AGCTCATCTGCAAGCAATTTTGTAGAAAGTTTGGGTTCTTJAGJCTGAAATTTTCCATGAAGTGATTTT TTTCTGTGCTTAACTTTCAGTTTAAAGACCTAAAGACCAAGGTTATCACATCACATATTTTGT
EST13518 2	39	A G C T T		G	ATGTTGGGCTTTTIG
EST13522 8a	45	C G			GAAACATCTCCAGTAGATTGAGGTTAAATGATTTCAGCATTTTJAGJCTTTAAATTTACCTCA ATGTTCTCTCGAGTCTGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13568 6	66	A G			CAGTTTGGTGAATCTCAACTAGGAGCTATTTTCCCCCATCCCGGCGAGTCTCTGGAGACJAV GTTTTTGAATGTCACAACTGCGAGAGGTTGCTTACTTGGATCTACTGGGTAGAGGCCA
EST13785 0	69	T C			CITTAAGGAAAGTGAGCCAGATGAATCCAAATGACCAACCTGGTTGAGAGCCATTTGGTCTAGGAGTAGA AAJTCJGCACACAAGGAATAAGGGAGAAGGAGTTGCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA
EST14038 1	101	C G			TTTCAAGCTAAGTAAATGSGT
EST14083 7	25	A G			AAGATTACGGACCATTAAGAACTGCCCCCGACCATACACACACAAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAAACJGJTGATTACGAAAGTGAAGGGCTACAGGG
EST14221 5	23	A G			TGATTACTA
EST14812 2	42	T C			CTCAACCATCTGTAAACCCGAGCCJAGJAGTGACCGGGACTTGTCTGCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAAGTCAAGAGGTTG
EST14815 3	50	A G A T A			CAATGGTGCCATGTGAACATATJAGJACCTATTCATAAAGTTAAATATCCCTTCTTGGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCACTGTCTTAAATGACCCGAACAGGAGGGTAGGAGG
					AATATCAATGCAATCTTGTGGCATGCTAGACAGAGGCAATATJCTTTTGAAGATCTTTTAAATAT ATTTGACTTGTCCCCCTTCACACTCATTTTAAATGTG
					TTGCATTTAGTACCAAGAGTGCCTTTCAAGTCAAGTCTTCTACATCTTGAATAJAGJATACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAACAAAT
					TTTTTCATATGGGTGATT
					TTTGTCTCGGCAATACATAGTGCAGCAATGCGAGTGTGCGCGCTCTCCCATGAAACCAAGTAAT TCACACAGACAAATGGCGCAACCACTTAAATAAAGTTGCCGCTCATACCCACCATCTGGTTJATTTCC
	128	A T A T A C T G G T T			GGTACTGTTTCCCGTA

EST15420 6	109 C A ...	GAAGAGACAA AGACAACAGA GGA	GAATAGCTGA AACAGAGATA TTATCTC	...	TTTAAACCCCAAGACTTGTAGTGTACGAGCTCCGATCATTTTCTGCTTATAGCTTGGATACTTA ATCTCTCCCTTTGTCAATCATATAGCCAAGGGACTCAJGGAATTTTGGCTGCTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GGTTTGGCCAT CTATAA	GATAGTTGATG TTCATTATTCC CTATAA	...	GTCACCAGCACTTTTATTAGACGTGAAAAGACAAAGACACAGAGGAG/CJAGCAGAGAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATATCCAGAGTCTTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGGCCAT CTATAA	GATAGTTGATG TTCATTATTCC CTATAA	...	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC/GAJTTATAG GGAATAATGAACATCACTTACCTACAGCTAAACCTAATGAAGACCAAAATTCCTCCAAAGGT
WI-16782	96 C T CACTGTAAGG TC	GGTGGAGTCT CTGTTCTCTCA	CTCTATCTTT CTGTTCTCTCA	...	CTTCTCTCTCTAGACGTGGAATACACACGATACAGTATCTGGAGATGTAGCAGCTGCTCTTGAC CATAATGGTGGAGTCTCACTGTAAGGA/CJTGATGGAGGACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAATTTGTGGGG
WI-16783	64 A G G	TCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA	G	AAAAATGTAACCTTAGAGGTTGCTCTTTTGTGTCTACTTTTCTGAGATGCTTTTACCTGAG/GJ CTATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C	CAGGACTTAAGGTCAITTTTGGCTGGAAAGACTTTTAACTAAAGGTACAGGCAACATAGGAT/CJGTGA CAGCACCACTCGGACCAAGGAGTGTGTAAGGATGCTACACTAGGTGCCCCCTTTTCTCTGGC TGCTCTGCTCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGACGACGCTTTATCTCCACTGCCACTGGGATCTCATTTTGAAGACTGTTTGTGACGCC TTTTCCAGAAAGGCCGCTGCGGGTTTCTGAACCCCTCTATGGCAATTTTGAAT
EST16089 9	96 C T	CGTCTGAAGTTTCTTTTATCACAAGTACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/CJTAAGAGGCCATCCCTGCCCCCTTTCTTTGCT
EST16100 1	24 C G	ATCCAGCTGTGAAGGGGACAGGAG/CJGJGTAAACACAGTCCCATTTTAAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACACACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGAATTTGCAG CTGGTTCTCCAGGAG/GJTTGGCCCGAAGCTGGCTCAGTTCACTCCAGGACCTCAGTC
EST16118 0b	119 T C	ATGGTATAACAAATCAGTCCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGTCTTTCCCGTGGC CTCTTAAACAACATAAAACACCCCTCTACGTTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G	ATGGTATAACAAATCAGTCCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTAAACAACATAAAACACCCCTCTACGTTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ...			AGCCAAATCAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTATCTAATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ...			CATTGGTTGGTAGGAAAGATAGTAGTGTGCAATAAAATGGTAAACACAGAG(G/A)AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGTAGGCAGAAAGTAGTA
EST16183 2b				GCAGGTAACACTGTGGTTTCAACACGTATTGTCTTTTCATAAAGAAAGAAATATCTAGTTG(A/G)GTAG AGGAAGGCACGTGTCTTCTCGGCCCTTCTTCGTTTCATATTTTATGTCACCTGTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	59 A G ...			AATCTTAGGCTCTTGGCTTTCAAAATCA(G/A)TACAGACAGATAAGAGCTTTAAGTATTTGCAATTT CCCCAGAGGAAAGTACGATCATAAACACATGGGTGCACATGCTCACGCACATGGTGTCTC
EST16229 2c	52 T C ...			TGTGAACCTGAAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTCTGGGAGTCTCCCTGTGCAGOC CTTGCCAGTTTCCACGAGCAGGATACCTCAGTAGCTGATTCAGACAGCAGAGGCTGCA
EST16229 2b	45 T C ...			TGTGAACCTGAAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTCTGGGAGTCTCCCTGTGCAGOC CTTGCCAGTTTCCACGAGCAGGATACCTCAGTAGCTGATTCAGACAGCAGAGGCTGCA CAGACTTTTCTCAGACCTCATTTGGCTGGAACCTGGTGCACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGGTGCATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA(G/A)GACTGTCC
WI-16816 124 A G TGGGGTTA		GGAGCCATTGT	GCCTAGATTTT	TGAACAAATCTAGGCTC
EST16269 5b	49 G A ...			GCCACTCTCTGTGCTTGTCTTGTCCAGCTGCTGCCAGTGCACAG(A/T)GTGCTAGGCTCATGG CAGAAGCATTTTAGCCAACTCTGGTGTCTCCACTCTCTCTTCTTCTCCGCCGCTGGGCTCACCAAC TCTTCTCTCTCAATC
WI- 16824b	83 G A ...			GTCAACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG(G/A)CTTACACCTTTAGCACGGATAGTTTCTGCTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI- 16824a	47 T C CAGCTGT	TGATGGTGTCTG	TTCTTCATAAG	GTCAACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGTTCACACCTTTAGCACGGATAGTTTCTGCTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ...			TTGCTTTTATTAATCCAGAAGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAATAAATGAAC(T/C)GGAAATAAGAGCATAAACGGGAACAGTAACATCA
WI-16857 47 G A A		CAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCTCAACACACACAAATAAGCAGCTAATGGCAAT(G/A)CTAGTGGTCTTCCCAA TTCAACAAGACCTGTGCTTCAAAATTTTCTTCIGATATGTGGAGAAATCTGCTCTTTATGTA

WI-17010	23	T C	TTCACAGGA	AATAACGGT	ATGTTTCAACAGGAAAGCCATGTCJATGACATTCAAAACACCGTATTATTAGAAGCTCATTTAAT
EST17127			CA	GTTTGAATGT	GGTTAATGCAGACAAAATCAAGGCTAACTAAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA
9b	74	CT	CACTGGCAC	GGGAGGGCAGG	GGTCCACAG
			AGACAGAT	GGTG	ATTCGTCCTCCAAACAGCATCCAGGCCGGGCATCTCCCGACGATTTTATAATACACTGGGCACAGA
			AATCTCTTAT	GGACTATGGCT	CAGAGTCJTGAGGAGCCATGGGGCACCCCTGCCCTCCCGAGGCTTCTTAAGTAACAACT
			CATCTCAAGCC	TATTCAGTGAT	CACGGGTTCATAAATTTGGTACAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
WI-17040	94	T C A		G	GAGAATTCCTCTATCATCTCAAGCCAGTCJATCATCACTGAATAAGCCATAGTCCCGACTCTCTTTTCC
			GCCAGGGAT		AAATCTTTCTCATATTGT
			TAACGTATAG	GGGGATCCCT	TTGTTTGTATTGTTTCTCTCTCTCCCAAGGGATTACGTATAGGTCJTTCTTAAACAAGGGGATC
WI-17044	47	GT G		TGTTAAGA	CCCCACTTATAGCTGACAGCAGCAGCTGCCAACCACTGACTCTCTCTGCAGATGGCAGGAATCGAAT
			TGGACTTGTC		CAAAAAGAAAAGCAAGTG
WI-17021	62	T A A C T	GCCTATACT	TGTAGATTAG	GCATGTGTGGAGCAGATCTCCATGTGAAGCCAAAAGTGAGCTTGTAGCCCTTAATACTCTTAAG
			ACTC	TGGCAGCTGC	CAGCTGCCACTAATCTACAGGCACAGTAACACTTTATACAGGAGCAGCATGCCAAAGTGCCCTGG
			CCAGAAAGGA		GAGGTGCCAATAAAATCAA
WI-17065	90	T C C T T	AAAGCATAAA	CCCAAGAGAC	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTCTACTTCCGGTA
			CTT	AATGAAATCCT	CCAGAAAGGAAAGCAATAAATTTTCJAGGATTCATTGTCTCTTGGGT
			TGTACAGCCA	GAGATGTTGAA	
WI-17066	32	A C T	ACATCACGTG	AATGTTCTGGA	TTCATAAGGTTGTACAGCCCAACATCACTGTTTTCJATTCAGAACATTTTCAACATCTCAAAAAGA
				A	AACTCTGCACCCATTAGCAGTCATTCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T G ---		...	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAAGCAT
WI-					AACTCTCTACACAGGCCCTTTCJATACATAGGAGTATATTTGGCCCAAGACTCACACTAGAAAGTGATT
17104b	108	T C ---		...	CAGATGAGAAGCTCATGTGGCTCATCTGCAAGCTTCCCTGATGCTTTGGAGCTTTCCCATTCATCCA
					AATCAGAAGCAGTCAGTGGCCCGCTTCCAGACGGCTTCJCTCTCTTTGTTAAGAAATTA
WI-					AGCGTCCCAACAGATGTTCCATCAAGGACTTGTGTTTCJGCTCTCTTCACTCTGCTATTTATAATAC
17114a	37	T C	TTTCCATCAAG	TTGTAATTAA	AGCTACTCTCCCAAGGCCAGATGCTCTAAGTGTCTAAAGAAGACTGCAGGCCCAATCAGAGTTACAT
			ATAGCAGAGTG	AAGAGAC	GGGA
			GATGAAATTC	TTCTCAGATC	
			AGATAGTCTTC	CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
WI-17150	76	T G C T C T T		G	TTCTCTTTTGJGATATCTTCCAGGATCTGAGAAGGGCTCTCTTGTGCTCTCTTAATTT
			CATTCTTTGT		GAATCGAATACGTCCATCTTTTGTAAAAATAACAAATAACGTTTGAJAGGGCAAAAAGCAAGATTCTG
			AAAATAACAA	CAGAATCTTC	TAAACCAACATTGGAAGGGGACAGAGGGGACAGAGGGGAAAGGGGCGAGATTTCACAGGTTT
WI-17163	43	A/G TAACGTT		TTTTGCCCTT	CCTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCCCTCA TGAGGACC	CCCTCAATTTT CAACTGCTTC	AGCAATGTCCCTCCAAATTTAGTATGATGAGGATATCAGTTTCATTTAGAGGCAATTTACTGG GGGAGGGGGTTTAAATCTCTGATGGGTTTAAATTCAGTGAGGAGTCCCTCATGAGGAGCTC/JAGAA GCAGTTGAAATTTGAGGG
WI-17180b	81 C G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCAC TTCCCAAGTCTGTCGCACAG GCTTCAACAAATTAQC/JG/AACATCTTGCCCATTTTGTTCATTATCCGCCACCCACACTGCACAGATGAG GGAGTC
WI-17180a	47 T C	CACAAAAATA TAGAGAATCC TGCA	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCAC TTJCCCCAAGTCTGTCGCA CAGGCTTCAACAATTAACCAACATCTTGCCCATTTTGTTCATTATCCGCCACCCACACTGCACAGATGAG GGAGTC
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC TCCA	CAAGAAATAT ATATTTGATTG TGTGGAA	TGAGGTAGCAGGGCATCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATJG/JTTCCACAGA ATCAAAATATATATTTCTGGTTGGAAATTTTAAATGTTCTTAACTATCTGCCCTACCATCCACCTCAAT TAATATTTCTTG
WI-17149b	79 T C	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGACGTTGCGTGGAA ACCCAAATTGCTAT/CJGTGTATGAACACAAAGGATGGGGAAGAAACACATTTCTCTCACA
WI-17149a	48 C G	CAAGGTTTGA AGGAGGAACA	CCACGACGTTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTGJTCATGACGTTGCGTG GAAACCCAAATTGTCATGTGTATGAACTACAAAGGATGGGGAAGAAACACATTTCTCTCACA
WI-17197	67 G A	GCAGAAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTTGCTATGTTGCTGGCTGGAGTCCAGCAATCTCCTGCCTCAGCAGAAAGTAGCTGGGGCTACJG /JGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAATAGAAATTTTACATTTTAGATGCGCA TGATTTTCAGTACTTTCTCCCTGTCCTCCCTGTTTACJTAATTTCTCAGTGGAACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAAATGCACATCC TTC
WI-17198 EST18753 8	38 A C 27 C T	TCCCTCTGTC CCTAGTTT CTACCCAGGCT GGTCTCAT	TCCATTTGTC ACTGAGAAAT GGATCGCATGA GCTGA	TCGCTATGCTACCCAGGCTGGTCTCATCTTCAGGGCTCATGCGATCCCTGCCTCTGCAGTGGCTGG GATAAGACACAACTGCCACCAGGCTGCCCTAGGAGTAGTCTTAAATGCTGATGGTGGG
WI-17108b EST19067 2b	74 C T 41 A G	GCCATTTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTAAACATACACCAGATGCACCTTGGTTTTTACATCTCTGTTGCCATTTCAGTCTCAAAGT AAACACJCTJGGBAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT ACACAAAAATTTACCATCTGACCATTTAAGGGTATAGTTTCA/JG/JGTGGCATTAAGTACATTTCAACT TTTTGAGCAACCCGCCATCCCATTCATCCATCCATCCGT
EST19067 2a	40 A C	CGTGACCATTT AAGGGTATAG TTC	AAAAGTTGAA TGTACTTTAATG CCA	ACACAAAAATTTACCATCTGACCATTTAAGGGTATAGTTTCA/JG/JAGTGGCATTAAGTACATTTCAACT TTTTGAGCAACCCGCCATCCCATTCATCCATCCATCCGT
EST19125 8	28 A G	CTGTTTCTCAGAGATGACATGGCCAAAC/JG/JGTCATACAATACAGATTATGATTTGGC TATTCACAAATTTACAGTAGTGTGTTTTTCTCTGAAAAA

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCCC	TGCTGTAA TTTGACTGTAA TG	GCCTTTATGTCTCTTTTAAACATCAAAATGTTTATAACACACTGTGATCCTTTTGTCTACCCCA ATT/CATTACAGTCAAAATTACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAITTT TTATTTCTCAGCTTACCATTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAATCTTTGCCTTT/ATAGGTTTGACAGTTTGTGTCTTCT T
EST23021 0	108 T A	...	GCCTTTGCCTA AGATTAATAGT A	ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAA/C/GJAATATTAG TAGTACTATTAACTTTAGGCAAAAGCCATTCTTTTG
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAA	AAGTACT A	TTTTTGGCTTGTCTGCAGAAATAGATGAAGAGAAAAATATACCAGATACTTTTGTCTACTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG/ACJCTTACAGAGGGGAAGGACGCTGAGGC CAAGAGTCTGGCTCACTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CTTCCCTCC TGTAAGC	AAAGGCTGTAGTTTGTGTTTTTGTCTTTTCC/T/GTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAAGGCCCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGCGGC TGAAGAATACCCACCTAAA
EST23733 9	31 T G TT	GGCTGTAGTT TTGTTTTGTT	TGCACITTTAA TCCCATCAAT	CTGACAGTCCCTGTGTGGGGGGTGTCCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGGGTCC GTCCGCCAGCCCTA/GTJCGGCTCGTCACTGGGCTTGGTCACTTTGTATTTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17470	83 A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGGA	TTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTAGCTAATGAATGCAAT/CJAGAGTATTG CCTGCAAAATAAATTGAGATCTATTTTAAAGACCTTAGAACAGTACATGGTGCATAG
WI-17519	55 T C A	TAATGAATGC TCA	TGCAGGCAATA CTC	TCCTTGATACAGGTAACAGTTTTGTAACTATTTCAGAACTTCACCTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/CJGTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3b	95 C G	TCCTTGATACAGGTAACAGTTTTGT/ACJACATTTATTCAGAACTTCACCTGTATCTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAAGTTATTGATAATGATGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581c	99 C T	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAAGTTATTGATAATGATGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAAGTT ATTGATAA	CGTCAATGTAA ATGCGCCT A	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAAGTTATTGATAATGATGAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCTTGTG TAAACACTCC	CATTCTTAG CAATAT	GTGTGCTGTAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCTACT TCCTTGTGTAAACACTCCCAGJATATTGTCTGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTG

WI-17623	46 T C	TGTGTTTAAATTTAAATTTCCCATATAATGTTGGTGGGCACATTTTCGCATGTGCTTACTGGTTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGCCTGACITTTGGAGTTTTTTGGT
EST26419 1b	46 T C	ATTTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGATTC/GGGCAGTCCAAACTTCT TGGGAGGAGTAAATTTTCATGTGTAATGTCATGATGGCTGTTGAGGAGGAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A A G	CAAGAAGTTTG GACTGCC	ATTTTCATACAGAGATACAAAGGCAACTATGTGCAGTC/AACAATCTGTGGGCACTCCAAACTTCT TGGGAGGAGTAAATTTTCATGTGTAATGTCATGATGGCTGTTGAGGAGGAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780	69 G C	TCAGCTTTAATTTAAGGGACATGTAAATAAAAAGATGATTTTGACAGGACAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACCAAGCAAGCAAGTCTGTTTCCATCTTGGCTTTTACCA CACTTACAACACTGATACCC
EST26900	39 A G	TACTTCAGTTTAAAGGCAATTTCCACACAGAGACTGTCTC/JAGGAGACGGGCACAGAACCAGACACC GTAGAACCACCAACCATGATGATGAGGGGAGCAGAG
EST27152	101 C T	CAAAGGATTTTATTTTGTTCCTTAAAGTAAATCTAGAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCTCTCTCTC/JTTTACATGGTGTACTCTTTTCATGTACACAT CATCGGAAAAACAGACTGA
EST27504 0a	33 G A A T T T	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACITTTGCACAAATTTAATTAATTTATCTG/JACATACAGTAGCATCACACCAGGAGTCAAT AATGCCACTTTAGCCAAAAGCTTTTCAGTATTTCTGTTACACATCTCTTAAACAAGAACCCATACAT GGTAAATTCATTTCT
EST27662	51 C T C T C C A G T C T G C	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTGT/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTAGGAATGTTC
EST27788	100 A G	ATTTTATAGGGGTACAAATTTCCAAAGGTGGTAAGGGTGAAGGAAAGGCGGAGGCGCAATACAT TATTGAGCTGAACAACACTTTACATTCAGGAC/JGJGCTTCCAGACAAGCCATGTAGAACCCAGCAT GCCITGGGACTGTGTGGAT
EST27828	58 G A A G A C C C C A C	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAACITTTCTCTCTGTTGGATCCCGAGTGACGTGGAAGTCATCAGAACCCCACTG/JGTACTT GGAGTACCTCTCTGCACCAAGATAGTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A A C A A T C	TAAGAAGGCC TATCCATT ...	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATCTG/JAAATG GATAAGCCTTCTTGACAAATTTCTGCCACCTCGTTTAAAGCATCAGAACTCAATCTTATCTC TCCCGCTTCCAAAGCTTTATTTGGCAATATGCTCTAT/JAAAGAAATGATCAATCTGTTGCCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACCGCTGCTGAAGGAGACTGCTGTGTG TCCACCTCTTATTCATAG
EST28036	37 T T C	

EST28483 7	31	T A	GGAGTAAAG GTGTTCTCT TTAAA	TTCTCGCAT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTAAAT/AJATGGTATAAAATAAATCGGAGAAACATTAAAC GGAGATGTACAGACAACAGACAGACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA AGAAATGGTCTAGTAATCGTTTCAGGATTCGGTGTATGGCCCTCCCTGTCTCTGAGACACTGCCAACCC CACAGCTGGAGGGGACCTTAAGGCACGTCATTTGTGATTAGA
WI-17724	50	T C	TGGGCTTCC TGTC	TGGGTTGGCAG TGTC	CGAGCTGGAGGGGACCTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68	T C	TGAGCCTGGGGAGAAAGACACAGAGAGTGAAGTGTCTATTAGTTACATCATCAAGGTGTACATCTG TTT/CACATGATTATGCGTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39	A C	GACCACAGAA GTGAAGTGT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACACAGAGAGTGAAGTGTCTATTAGTTACATCATCAAGGTGTACATCTG CTGTTACATGATTATGCGTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53	G A	GGACAAACA CATTAAAGCAT CA	GGTATTGTGA TTTGAGGAGTT AGC	TACTGAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCTGTCACCT[G/A]GCTAACTCCT CAAAACAACATACCCCTTATTTTAGCCATGAAGAC
EST29128 4	58	A G	CTTTTGAAGGACACACAGTCTTTGGACTTAGGCGCTACCTATTCACAGAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCTGTGAAGGACCGTTTCCAAATGAGGTACAGTCACAGGTTCTGAGCAGACATGA GTTTCTGGGGACACT
EST29912 3	103	C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGT TCATCTCTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCTTCACAGAGAAATGAGACACTTACGCCATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	TATGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTCTCTGACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99	A G	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTAATATTC[A/G]GGATTAAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86	G A	CTTTCCATTTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAGAACCCAGA GTTTCACAAATAGGTAGTGG[A/AT]AACCAAGGCTCACTTCCCTTCGGTGAGAACTTCGTGGGAC
WI-16260a	59	G T	CAAGAAGAAA A	CTACCTATTT GTGAACCTCTG GGT	CTTTCCATTTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAGAA[G/T]ACCC AGAGTTTCACAAATATAGGTAGCGATAACCAAGGCTCACTTCCCTTCGGTGAGAACTTCGTGGGAC AAGAGAAACAGAAATATTGTCTTCTG[A/G]CGCTGTTCTTATACCCCAATATCATAGAATT GTTGTGCTCTTATATGTTGAGTTCAGGTTCAAAATCTTTTGTGTTAATCAATCAATGAATTACCTGAATT TTCTCTCTTGTGTTCAAAA
WI-17835	30	G A	TTGTCCTTCT TG	TGGGTATAGG AACAGGC	

EST31951 4	87	C T	GGTGTCCAG CCAACA	CCACCAAAAT CACTOC	ACAGCAATTAATTATGTTTACTTGGTAATATCAGAGACTGAACATTTTCACCTCTTTAGCAATGACA TCGGGTGTCAGCCACAC/CTGGAGGTGATTTGGTGGGAATTTCTTATCACAATTTCT
EST31968 8b	95	T G		---	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCTTAAAGATTTGGGGGGGGTGTACTATAGT GCATTTTATAATGGGGATTTCTGCTTT/GAACTGCCCACTGATCTTACATGGGAAGGTGCAAAAG ACAGTGGTACTGCTOC
EST31968 8a	75	T C T	GCGGTACTA TAAGTGCAAT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATTCTAGTAATCTTAAAGATTTGGGGGGGGTGTACTATAGT GCATTTTTC/ATTAATGGGGATTTTCTGCTTAACTGCCCACTGATCTTACATGGGAAGGTGCAAAAG ACAGTGGTACTGCTOC
EST32063 2	103	C T		---	TCATGGATGAACAGAGCTACCATGCCACATCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGTT/CTTTCAGGCCCAATGAAATAGCAACGCAC AGTCATGAGCACTCGG
WI-16303	65	A G		---	AAGCTTTCCAAAGCATTCAAAAGGCACTTGGGTGTTGTGCTCTAAGTTTCTGTCACCTGCAGCCCTC/AG TTCGTGATTAGGGAGCACCCCAAGCCCAAGTAACAATA/TGGTTCTTGCAG
WI-17800	29	C G	GGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGAGCACAAAGAGAACTCACTC/GAAGACTGGGATTAATTTAGGAAATATTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCTCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AACTGTCACTCCTAAAGTCTGGGATGACCTTCTCT/GATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAAATCAGAATCCCTTTTGTCCATCAATTCAGCTAACTCCAGCTCAAGCTGAATTAATTTTCTTCT GTATCTGATGTAGTTAAACCATGGCCTGTCTATGATTATATGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAATTAATCTTGGTTTAAATCTTGGCAGCAAGCAAAATATTA/CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860 4c	121	T A	TTTCCAGCAA AGCAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTGTGTTTATAGCTACTCTCAAAATTTGTT/ATTTTGTGTGATTAGTGACAACG GGGAATCTACAATGCTCACATCACAGTAACTACCA GAAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACCAAGCATGATC AATGCCACAGAG/GA/ACTGGATGCCAAAGAGTATGG GAAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCTCTCACCAAGCAT/GA/
EST33301 4b	80	G A	TTTATAGCCT ACTTCTCAA	COGTTGTCACT AATCACACAA A	ATCAATGCCACAGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	63	G A	AGCGTGGTTT CAATACTAAA	CTGTATTATT GTTAAATATT GCATTGTT	CTATCCAAAGATATTATTGCAGCGTGGTTTCAATAC/AAACAG/ATGTAAACAATGCAAAATT TAACAATAAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATCTTTGGCA

WI-17904	50	A G A C A C	AAAGCATGAC AATAAAATGA	CGCTTATGTTA ATAGTAATTCC GG	CAAGTGAATATTGATACATGGTGACAAAGCATGACAATAAATGAACAC(A/G)TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACACAAATGA GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T(A/G)GATTTTATTAGTTGTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAAATCACAAAGT
EST34149 5	69	A G A T	TGCCAAATAC TCAAGTGTGA	AACACTAGCG AGAACAACTA ATAAATC	TGGGAAAACATAAGTTAACTCAAGAAATATATCCAGTCTTATGTTACTAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC(A/T)ACAAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
EST34343 8	95	C A	GGACCATATG ATATAAAT	...	GGTACACAAATTTTAAATGGAAGGAAACACAGGTAATGTTGAAAGAACATCAGTACAGCTGGGAGACAGG GAGGGACCATATGATATATACTCTCTAAAAGC(C/T)GGAAGGAGTTATATCACATAAATTTCTGGGC GCTACAGAAAGTTTTCATCA
WI-17982	98	C T C C T A A A G C	ATATAAAT CCTAAAGC	CGAAATATG TGATAAAT CCTCC	CTCAGTAACTCCGGTGTATAATCTGCCATTTATGATTTTATGATAAACAACCTCTCATTTGTGA AAAACAGCTAAGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATG(TA/C)CTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17993	118	A C	GTAGAGCGGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCAGAAACCCAGGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCAAGGCCCTCGCAGT AGAGCGGAAGGGAACAG(A/G)GCTGCCCATGTGCCCTGCTCTAAAGACGCCACCCCTCAGGTTGATGT CACTGTGGGAGACGGGT
WI-17996	84	A G A G G G A C A G	GTAGAGCGGA AGGGAACAG	AGGCACATGGG CAGC	ATTCTTTTATAAAAACACCCATGTCCCTAAAATG(TC/G)ATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-17136	33	C G	GTAGAGCGGA AGGGAACAG	AGGCACATGGG CAGC	GCCACTGAAAAAGGTGCTCTTCC(A/C)GTTCTTAACCTCCCTGGACTCCCTCATTTGGAACTGAAGTCT ACAGATGTTTCAGCTGGAGTAGTTTAGACTTTTGCTGATTTTAAAGGCAGTGTGCTCCAGGAT TCAAATCTTAATCA
WI-18041 EST35164 8a	24	A C	CACAGCCCTGC CAGAGCCCTGC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTACAGAGGCCCTTCAAGCAGACGCCCTGCCCC(A/G)TCTTGA GATTCAGAAATCCAGAGGTGCTCAGTCTTGGTTAGGTGCTTCTGTGACATTTCTCTTG AGCGAATGAAAATGCTACAGTCCCTGAGTTCCTTTCATGTAAGAAATCTTGGTTACACATCTTAG A(G)ACAGCAGAGCTGCTCAGGAGGGGTGTTTAAATGTCGTATGCTCAGCAGCAGTGTGCTGGC ATGCCCATCCATGCTTT
WI-18052b	67	A G	CCTGAGTTCTT TCATGTACGA	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGATGCTTTCATGTACGAATCTGCTGGTTACACATCTT AGAACAGCAGAGCTGCTCAGGAGGGTGTGTTTAAATGCTGATGCTCAGCAGAGTGTGCTGGC ATGCCCATCCATGCTTT
WI-18052a	50	T C A T C	GGGAGTGGG GAGTAAAA	CGTCAACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGAGTGGGGAGTAAAG(A/G)TGGAGGAGGGGTGACG CATGCGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAACCCCTGTGGGAGCTGCTAGCTGTATTTCAGAGAGATGTCAC AATCATACCACCTGGGAGAGAGTAAGACACAGTGTCTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TTCCAGTTGGT	OCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGAGCAGGATCTTTGATCATGGGGTGGAAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAATTTTCCAGTTGGTAAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A C G T G A T	AACCCACTAC TTACTCAGAGT	AAAACATAA AGAACTGGA	AAACCCACTACTACTCAGAGTGTGTAT/CJATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTATTAGTTTGTATTTCTCTACTCAGAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C T	---	GGTTTT	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTTTTGTAAATTAATACTACTATGCCGTG TTTGACTTTTATC/TJCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTCTCTCTTTGGTGTAT
WI-18080b	65	G A	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTTTTGTAAATTAATACTACTATGCCG/ ATTGTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTCTCTCTTTGGTGTAT
WI-18080a	41	T C A G T C T C	GCAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAACA	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCT/CJTGTAAATTAATACTACTATGCC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTCTCTCTTTGGTGTAT GTGGGCATCCTATAAAGCAGCCATGTGTGAACCAATGATATGCACAGAAAGCATCTCTG/AJ TGCTTTGTACACGGGTTTCTTTCAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18086	63	G A	---	---	AACTACATAGTATGGTGCTGGCTTGAATCAATGGGTAAGCCCTTTAGTGTACCTTTGGTATTCCTC TTCTCTTTGGTATGAAGACAGACCTCTGCTGGAGGACTATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115b	71	C T	---	---	AACTACATAGTATGGTGCTGGCTTGAATCAATGGGTAAGCCCTTTAGTGTACCTTTGGTATTCCTC TTCTCTTTGGTATGAAGACAGACCTCTGCTGGAGGACTATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70	C T	TT	A	TTTGAAGAGCCTCTGTAAGGCAAGGATGCATCAAAAATGGCTTTGAGGATTAATCTCTCTTTA GGTAAATTTGCA/GJTAAGAACATAAAGCATTTTAAAGTCCACTGCCGCTTAAAGAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCGGGAAGCTC/AJTTGGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18136	78	A G	---	---	TGAAAGAAAGTCGACACAGCGGACACTG/AJTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA
WI-18169	115	A G A A G C T C	CCATCTTTCCG	GAGTCTGCTT GTGCTCCA	---
WI-18190b	26	G A	---	---	---

WI-18190	62	G A ...	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT	... TTG	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCTATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCTGGCGA GACAGTGAAACAACTTGAACACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACCGTA TGTGTCTTGAAC ATTATACAAAGCATTTCCTGAGTACAACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCTG/GAGTGTGGGGGAGAGAGGGGATTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAAATCCCTTC CATTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA CCCTGAAACCTTTATTTGAAATGAAGTTTTGCTCAGAACTGGGCGAAGCTTTTCACATTCTG AC
WI-18181	100	A C CAGATC	AGCAGAGTTC CTGCCCTC	CGTCCCTCTCT OCCCC	...	TTTAAAAATGCTTAGAATTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C]CTGTCTCACTAGTCTATTACCTCTGTGGGCAATTCGGCAGAAGTGGC AATATCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTTTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACCTTATCTCACCAATCTTTCAAGCAAGTGAGGGTCAGAATGTTCTTGCCTATATC TGCAAGAGATCGAACAAAG GCATCAGACATCACCCTCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATCCACAT[C/C]TGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]GCACAAATGATGCAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18215	78	A C TCGCCTC	AGCAGAGTTC CTGCCCTC	CGTCCCTCTCT OCCCC	...	CTGAGCCTCTGGATATGGTTAGTGTCTATCATTAATTTTGGAAAGCTGTCAGCTATGTTATTTTC AAATAGTATCTTCTGCTCCCTTTCTCCTTTTCTGGGATCTCATCTCTGCAITGTTATA AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAAACAAGAGG A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAGAACATAATTTTTTTTGTGAT TCACA
WI-18232	60	T A A A	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT	...	TTTAAAAATGCTTAGAATTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C]CTGTCTCACTAGTCTATTACCTCTGTGGGCAATTCGGCAGAAGTGGC AATATCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTTTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACCTTATCTCACCAATCTTTCAAGCAAGTGAGGGTCAGAATGTTCTTGCCTATATC TGCAAGAGATCGAACAAAG GCATCAGACATCACCCTCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]GCACAAATGATGCAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18256c	119	C T ...	AAATAGGAAA TATGGACTATC	TTTATGCATCA TTTGTGCA	...	CTGAGCCTCTGGATATGGTTAGTGTCTATCATTAATTTTGGAAAGCTGTCAGCTATGTTATTTTC AAATAGTATCTTCTGCTCCCTTTCTCCTTTTCTGGGATCTCATCTCTGCAITGTTATA AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAAACAAGAGG A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAGAACATAATTTTTTTTGTGAT TCACA
WI-18266a	97	C T T TCAAA	AGCAGAGTTC CTGCCCTC	CGTCCCTCTCT OCCCC	...	TTTAAAAATGCTTAGAATTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C]CTGTCTCACTAGTCTATTACCTCTGTGGGCAATTCGGCAGAAGTGGC AATATCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTTTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACCTTATCTCACCAATCTTTCAAGCAAGTGAGGGTCAGAATGTTCTTGCCTATATC TGCAAGAGATCGAACAAAG GCATCAGACATCACCCTCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]GCACAAATGATGCAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G A A	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT	...	CTGAGCCTCTGGATATGGTTAGTGTCTATCATTAATTTTGGAAAGCTGTCAGCTATGTTATTTTC AAATAGTATCTTCTGCTCCCTTTCTCCTTTTCTGGGATCTCATCTCTGCAITGTTATA AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAAACAAGAGG A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAGAACATAATTTTTTTTGTGAT TCACA
WI-18330b	66	A G ...	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT	...	TTTAAAAATGCTTAGAATTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C]CTGTCTCACTAGTCTATTACCTCTGTGGGCAATTCGGCAGAAGTGGC AATATCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTTTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACCTTATCTCACCAATCTTTCAAGCAAGTGAGGGTCAGAATGTTCTTGCCTATATC TGCAAGAGATCGAACAAAG GCATCAGACATCACCCTCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]GCACAAATGATGCAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT

WI-18330a	49 GA	TCCTGTAA AATCAGGGAT	AGTCCTGACTC ACTGCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTGAAGAAATCAGGGATAGA(GA)CTGAGGAACAAGA GGGATATGTAGGCAGTGTAGTCAGGACTATGCAAAACATAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85 T C AGA	AAATTCAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGATTTCCTCATTGAGGCCCTCCATAGGCTGCAAAACATCAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104 GA TT	AACACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGATTTTTATACCTACACAAGTAGGAGGAGGAGCTGGGGCAGTTTCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTGCTTAGGCTAGTTGAGCTGAGCCATTGTAATCGGAGGGCAGA GT
EST37624 6b	102 GA			GTGGCAAGAGGAGCTAAACACACTCATTTTGCATGAATCCCAATACGAACAGTGCACGCTGATGG OCTGCAGTCTCTGCCGTGCTGGCTCTCGACG(GA)TTTCATCTACATGGCTGCTTTTGCCTCC TCTGACCTCCCATTC
EST37624 6a	58 C T			GTGGCAAGAGGAGCTAAACACACTCATTTTGCATGAATCCCAATACGAACAGTGCACGCTGATGG TGGCTGCAGTCTCTGCCGTGCTGGCTCTCGACG(GA)TTTCATCTACATGGCTGCTTTTGCCTCC TCTGACCTCCCATTC
WI-18357	89 C G GCATCAA	CCCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTTACCGTCTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTGAGA TAATCCAGCCCTTAGCATCAA(C)GTCTCCTCAGTCTTTGAGTCTTCCAGCCAGGTCCCAAGCTT GTGGACCCAGAGACAAGCC
WI-18012g	117 A G			TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTGGTGAAGTGTTCCTGATACA CGCTGACGTTTGGAGGG
WI-18012f	113 GA			TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTGGTGAAGTGTTCCTGATACA CGCTGACGTTTGGAGGG
WI-18012e	112 C T CCTT	GCCACTTTGC CCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTGGTGAAGTGTTCCTGATACA CGCTGACGTTTGGAGGG
WI-18012b	46 T C			TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTGGTGAAGTGTTCCTGATACA GCTGACGTTTGGAGGG
EST38390 4	75 A G C T C T G C A T T G	GCAAAAAGGA CTGATTAATAA ACTTAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATGCCAGATCTACACCCAGAGTAATCCCATGGTTATGATGGCAAAAAGGACTC TGCATTGT(GA)GTAAGTTTATTAATCAGCTGACTTTAGCATTTGGGAGATTATCTGGAT

EST38878 9	47 T C ATCTAA	AAACATCAIT ACTAGCCTAG CA	CCTTCAATAAA TCTCATGTCT CA	CCAAATGAGAACCAAGTAATTAACATCACTACTAGCTAGATCCTAAATCTGTGAGGACATGAGATTT ATTGAGGGGAATCCTCAATTAATATGAACAATTTCTTGAGAAATGGGAAATTTGAAACATTCCTC TTATTCAATGTCTATCTACACATTTCTTATTTTATTTTATTTTCTCAATTCCTCAATATCGGATTTGTG TCATGAGATAATGGCTGAGGGAGCTGGCAGCGAGTCTTCTCA[GC]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TGTCATCTCAC ACATTTCTTTAT T	CGATATTTGAG AAAGTGA AAA CAA	TTATCAATGTCTATCTACACATTTCTTATTTTATTTTATTTTCTCACTTTCTCAATATCGGATTTG TGCTCATGAGATAATGGCTGAGGGAGCTGGCAGCGAGTCTTCTCAGGCTCCCTGGATAGCTAAATTT TA
EST38882 6a	35 T C TTTT	TGTCATCTCAC ACATTTCTTTAT T	CGATATTTGAG AAAGTGA AAA CAA	TTATCAATGTCTATCTACACATTTCTTATTTTATTTTATTTTCTCACTTTCTCAATATCGGATTTG TGCTCATGAGATAATGGCTGAGGGAGCTGGCAGCGAGTCTTCTCAGGCTCCCTGGATAGCTAAATTT TA
EST38909 5	47 A G GCTAAAACG	GCACAGCATG GCTAAAACG T	GGTATTGTTG ATTCCCATCTT T	GCACAACTAACTTTCAITTTGTTGATTCACACAGATGGCTAAACAG[AG]TAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATCTGCTGGAGGGAATATAAAATTT AACTGAATGGCAGTGAAACACACTACACATCAAACTTAAAGGAAATGTGTTAGTGTGTTGACGTTGAG GGAACTTTATAACCTCAC[AG]CGCTTTTTCACAAACACAGCAGACACAGAGATTTCCCACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G CAC	ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	TAAACATTCCTATTGAATTCCTTTGTTGGG[GC]GGGGGGGGTGGAGATTGCACTGCTCAAGATAAA TATCAACAATATATCAAAACTTCAAAATTTGCTATGCATTACACACTGACATGAGCCACAAACATT CCTTTACAGGAGCTGTAC
EST38955 5	30 G C GGTGGG	TGAATTCCTT GGTGGG	CACGTCAATCT CAOCCOC	TAACATTCCTATTGAATTCCTTTGTTGGG[GC]GGGGGGGGTGGAGATTGCACTGCTCAAGATAAA TATCAACAATATATCAAAACTTCAAAATTTGCTATGCATTACACACTGACATGAGCCACAAACATT CCTTTACAGGAGCTGTAC
EST39002 0	42 G A TGACC	GGACCTTTGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCTGGGAGATCCCGGACCTTCGGTGAC[GC]CAGGCTCCCTGGCAGGGCTTGG CCCTGACCGGGCTCCCGAGCTCGGCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G CCTAAGGAAT	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCTTAAGTTTCCGGTCTTCTCAGTCTGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGTC AAAGACCTAACTTCTGGA
WI-16398	90 T C TCA	TCCCTATTAT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCAATCAACCAACATATAGAAACATAAAGAAAAATAAGATATCCACCCTAAAT CCCTATTATTCATGATATTTTCA[GC]AGCAACTAGTATATATATATATATATATTTTTTACAAACCAT TCAGTTACAC
WI-16403	69 T C ACT	CCTTTGCTCT AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCACTTTCTCACTTCTGAGTTTCTGGTCTTCTCAATTTTAACTT TTCCTTTTATATAGGGAATTAGCCCTTAAACTGTGTGATACGTGCGAAAAATTTCTCCCAAGTT TTCCTTTTATATAGGGAATTAGCCCTTAAACTGTGTGATACGTGCGAAAAATTTCTCCCAAGTT
WI-16406	24 C T AGG	GCCTTAATGGC TACAGAAAGA AGG	CCAGAACCCAG ATGTTTAA AA	GCCTTAATGGCTACAGAAAGAGG[GC]GGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATATGCTATTAGCAATAGGTCCTGAA

EST39236 0b	57 C G G T C T	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAAATAAACTTCCTGTCTAAATTTTCCAA/C/GIACATATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAATGAATGAGGTGCTC TTT
EST39294 4	63 G T G G A T G C C	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCQ/G/I TTCTCGTACTATGTTTAAATTTGCTGAGCCAGCAACCTCGAGTTACCCGGCTTTTACCCACGGCC AGCTCTGCTGTCTGCAT
EST39366 2	72 T C			AGAAAACATTCTGTCTGATCAGAGGAAGATGATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT/CJACACTGAGAGGAAATGGAAAAGAAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGTTTCA
EST39371 9	86 A G G G T G A G A G G T T	CATTGGATT AATTCACATTT	TGATTGAGAC AATTCACATTT	AAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAATTCCTCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG/G/AAAAATGTGAATGTCTCAAATCAATGCTTCCTCTCTAAAGATT GACATTGCCCAACCTGC
WI-17177	23 A G			ACAAGTGACATATCCAAACCAACQ/GJTCATCCCCACCTGTGCCCTATTCTTCTCTGTGTTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAACTGCACGAAGGCTCCCGGTACTCCTCCCTGGAA G
EST39428 8	31 C T A T T T G A T T	GCTCCCCACA TAACTGATGTT	GGTCCCTATG AAGCCACC	AGTTCTCTGGTTGCTCCCCACAATTTTGAATTC/JGGTGGCTTCATAAGGGACCCAGGATTCGCAIT TTCTGGGTGGGGCTTAGGTAAATCTGTTCCTTTGGTCCACAGAGCAAAATTAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45 A C C	GGCAGAGGAA TAACTGATGTT	CAGGGTCGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGCAGAGGAATAAATGATGTT/CJCAATACCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCGGGTGAGGATGCTCTGGG
EST39446 7b	117 C T G A G T A A	CTACTGACAT AGGACTTCA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACACACGTCACCTTTGGAAGAAAATACAGGAACCTATTATAT ACGTAAATCACITTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA/C/JGGTTTATGTCAGT TTCCAGGATTTCTCC
EST39465 2	80 A G G T G G C	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACAGACAGAA TGACAGAGGGTGGC/MGJHAGAGGGGCCGAGATTGGGTTCAGGGCAGAGAGGTGGAGAGCAG
EST39501 0	81 A G A A C A T T A G	AAAGATTCTT GTAGACATCT	CACITTCGAAT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTGTTTCAGACATCTTGACCAAGCCCTAAAGATTCCTGTAG ACATCTAACATTAG/GJTAGCCTTCAGAAITGCAAGTGCAGTTCAAGTCAACCAATTC
WI-18387b	84 A C			CACAAATGGGACTGCTGAAGAGTGGACAGTGGACCTTACTTTGGTGACCCCATACATTTTGGTCA CATGCTTTAGCCCATAC/CJCATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGATG GCTATGTAGACATAAAGA

WI-18491	109	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCITGTAATCC	CTAATCAGATGAATACATGGAAGGCGTTTAGCAGAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTACTATTATTAAATCCAGAAATGAC(G)AGGATTACAAGAAATGCACA
EST50757 b	79	GAGCTGAGG CTGCTTCT	AOCCTTCAOCC GGCC	AGCCCTCCACTCCACTCTGCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTTTTATAT GTGACGGGCGCTGGGCGGGTGAAGGTCAGAGA
WI-17675	103	GGACATTTGG ATGTTGACTT	GGGGAOCCOCC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTCAACAGGTGCTGAAGAAAGTGTCTTCTGTTTAAAT TGCCAAAGCAGGATGTGGACATTTGGATGGTGACTTTCGCTGGGTGGTTCCCATAGATTACCAT
WI-16543	67	AGATAAACA CATTTGGGTT	GATTCATCATTT ACAGGGGACTT	TGCCCTAATGGTGTCTA GATCCATTACCTAGGTGTAATAATTCCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTGG GTTAAGTCCCTGTAAATGATGAATCAAGAATCCTCAAGTCTGCTTGCCACCAATTTAATACGTATT
WI-17687	107	GCCAAAAAGG TTGGGAA	TTACTTTTGTGTA CCGACCAGCA	TTTGTAAAGGCTGAAGTT ATCTGAGATGGAAGAGATTTCATCCCAAAACCATCTCCOCTGACCCCGAGTCCCATGGAATAATGTC TTCCACAAAACCGGTCCTGGTGCCCAAAAGGTTGGGAA(G)GCTGGTGGTACAAAAGTAATT
WI-17690b	79	AGGCATTTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGTAATC	ACAACATGTGAAAGAGATATGTTGTCTTACTACAGTGGAGGCATTTTCTAGCTGTGTTTGATT GGCTTCCCTATAGGATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	ACAACATGTGAAAGAGATATGTTGTCTTACTACAGTGGAGGCATTTTCTAGCTGTGTTTGATT TTTGGCTTCCCTATAGATTCAAGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG GATCCAATCTCAGTGTCTAACTCATCCACAGATTTCTGAAGTGGAAACCACTCCGACCCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGCGAGCGGAAAGACAGTGAGCTGTTCTGAG
EST51717 a	39	TTGGGAAAGG GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	CTGGATTATGGCTCAAA GATCCAATCTCAGTGTCTAACTCATCCACAGATTTATCTTGAAGTGGAAACCACTCCGACCC CAATGGCAACATCAOCCACTACCTGGTTTCTGGGAGAGCGAGCGGAAAGACAGTGAGCTGTTCGAG
EST53012	97	TGGTCACTTTG GGGCG	GGCTCTGCCCA GGCC	CTGGATTATGGCTCAAA TTTCCAGGTTGACAGGTTTATTCACCCCTTCCATCCCATGGCCACCCAGCGAGGAGGACAG GTGTGCTGGAGTGTGGTCACTTTGGGGCGCTGGGCTGGCAGAGCCACTGGGTTTACATTTCTCTGT GGGCGAGTGTGGACAC
EST53349	96	AGTCAATG GTAC	CATCTGGATAT CTTGTACATTT	AAACTGCAATTAACAAAACACAGAAAGTCCAAAGGCTAAAGTCTAAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAACATGTAC(G)AAATGTGACAAAGATATCCAGATGTTTAA
EST53389	74	AGAACCTTAA GCA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACAGACTGAGAGCGCCAGCCAGCGAGGACCTGCAGAACT TAAACAC(G)GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAAGGAGATGGCC

[illegible]

TGR- A003P30	117	C G	ACAGTTCAAAGGAGAACCTTCCTTTGTTTAAATGCAGCTGTGCTCAGAGCCTGTGATTTCTCAGGA AACCATCTGGGTTTAGCCATTAGAAAATGCAGTTAAAGCAGTGTCA/C/GACTGGCTGCCTGAA GGTACCCITGGAGATACT
TGR- A004S34	156	C T A	GCTTGCTTTTATGTTAGGTTGGGGAAAGGAGGGCTGACAAACGACACATCTGGACACCAGC AAGGTCACGGGGAGGTTTGCAGAACTTCTTTGCTCTGGCTACAGTCTGTGACATAAGCCA AACCTCCTATTCTCTATAAA/C/TCTTAAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C	AACAAGGTAACTCTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT/C/JAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAAATATGACTTAGCAAGAAACAAATATAG
TGR- A004T44a	69	G A TGA	AACAACAGTGAATCTTTTAAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCAAAATGAT TGA/GATATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAAATATGACTTAGCAAGAAACAAATATAG
TGR- A004V08	60	T C	GGCATCTCTT	...	CCTACAACTCTATAATTAATGCAAGGGTTGGAGGATGCGAGGAACAGGCAATCTCTTAT/C/GCC TTTTGTGGGAAGATCAATTTGGGTGCATGCACCTTAGGGGACAATTTGGGAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TGR- A004V26	125	A G	TCTAGCTATAAGACACAGATTTTAATAATCTAGATATAGAATATCCAGAAATTTCTATTGAATTGA CTGATTTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTTATCTTCACATGA/J/GAAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTTGCTTAAATACTGTATCTATTGG
TGR- A004V28	29	A G C G A T C T C	CCAGGCTATAATGTTGTGGGTGCGATCT/C/GGCTCCTACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCTCTTGTAGTAGCGGGACTACAGGCAACCCGCCACCTAACTAAATTTTIG TATTTTITAGTAGAGACATTTGATTTTTTITAGTAGAGACAGG
TGR- A004X20	25	T C G A	TAAAGTTTCCCTCTCTCTCTAGGAT/C/GTCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGCTTGGCTTCAGAGGATTTGATATTTTGGAGTGGTACCTTTGTCTGTGCTTTTCA GACCAACCGCTCTCTTCTTCAAGGCTTCTTCAAGGCTTCTTCCAAAGGAGTAAATCATCATCATGCTCCAATC ATCATCATGTCTCT
TGR- A004X30	26	T C C A C	TTTTGAAATCTAGAGTAGAACCCACT/C/JACTAGTAATACTGTATAAATAAATAAGATGTTTT AAACACTTCCATAAAGAAATAGGGTGCCAGCTCTTGATTTCCCTTAGGGATAAAGATATCCAT GTTAGGATAAAGATATCCATGATC
TGR- A004Z04	102	T G A T G C A A A A A C T	CACGGTATATGCTTATATAGTATATACAGATGCTACACAAATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAACTT/GTGTCTTTCATGAATTTCTAATATAAGG ACTGTGCTTCTTCTATATTCATGATGACATATACAAAATACAGTCTCTTTAGTGAITTAAGACGTC TCTTTAGTGAITTAAGACTG

TGR- A004Z19	85 C T	GAGAACACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTCTGCCCTAGCTTGAGAGACAACATGC AGCATTTTCTCTTTTCTCTCTCCCGATGACCATCTTTTGGGCTGGGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCC3 GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGGGGGCA GGGTGGGGGAGGTAGGAGACTTCTGGACCGGAGGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TGR- A005D17 c	81 T C			TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCTCTCTGTGCGAGGATCTCTCTCTGGGCAC GGGTGGGACCCCTCTCTGGATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCTCTCTGTGCGAGGATCTCTCTCTGGGCAC GGGTGGGACCCCTCTCTGGATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TGR- A005D44	97 G T	TTAACTTATT GAACCTTAAA CTGTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACACAATTTGGTCACTCACTGAACCTTGGCTCCAATATATTTCTATACAATCTT AACATTATTGAACCTTAAACCTGTGTACACTGTGTGTGTGGCTTTAAATAATAGACAATGATTTTG TCTATTACTTAGTGATAGACAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TGR- A005E31b	27 G A			GGAGTCAAAATTTATAACCGGCTCTG/ACTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCCTGCCATGTGGATAGTACTCTTTGCCCTGCTTGGCCCTACAAAGCCACCTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TGR- A005E39	182 G C			CTCAGTGTAAAAACTTTGTTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAGTG CCAGGCTGGATGGTGGTGGAGACAGAAATGACCCCTGGGCTCTTATTTTGTCTTTTCAACAGAAC CCACAGATAATTCGGGTATGTCATGAGGACTGGGGATGCTCTTATTTG/CGGATGTCTCTATTTT
TGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTTGTATCTTAGTAAGGTTACTGCACTTACAGAG/AGTCTCAATTTCCCTGATTAGGA AGGCGATGCTAATGGGTATGCGATAGGTAGTAAAGTATAAAATGTTGTATTTAAGAGAAATCCCAACAG CTTGGTATAAGGAGAAAAAATAATGGTATAAGGCAAGAAAAATAAG
TGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATAGTATAGCCTACCGTTTGTAGCACCTACTCGGTATCAGGACCTGACTCGG TGCTTTAC/AGTACATACCTACAGCCAGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAAG/CTTGGCTTAGGGTGTCTCCACAGACAGACAGATCTTGAACCG ACTCAATTCCTGTGTAAAGAGCACCTTGTCTGTCTTACAGGACCTCCCCAAAGTGTGCGAGATCTAT ATAGATGCTGGATTAGTTCCTTTGATATTTGTAATAATTCCTCCCAAGAGCGGCATATGAATCTGCC

D63807	101	C	---	---	---	CAGCGAGGACTTCAGTGTACGATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCATCTC ATTGTTAGAGGGAGTGATTTTCTGTTCCTGTTCCATCTGGAAGAGGACTTTTGTTCACAATGGATCAC AATGAGAGGAGTGTCTTCTCTCCCGTGGCTCTCGGTCTGGAGGGTGACCTGTCCAGATGAC
D90145	21	T	C	---	---	TGGGAACATCGCGTGGACCTCT/CJACAGCTACCTCTCTATGGACTGGTTATTCGCAACAGCCACA CTGTGGGACTCTCTTAACCTAAATTTAAATTTATTTACTATTTAGTTTATTTATTTATTTATTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTTCCCGCTGTCCCTCCACCTTCCTCACAGTGTG
EST14035	59	T	C	---	---	TCTGGTG ATTATCACTCTCAAAAATTTGGTGTGTGTTAAGTACTTTCTTATTTATGAGCCCTTC/CJGAGGA CCAGACATGTTATTTATCAAGCCCTTATATACCATCTAAT
EST16668	71	C	T	---	---	GCATTTAAATTCACATTGAATCATTTACTATTTACTATTTAGTGTTCATACAAATTCAGTATCAT ATGTC/TGTAGATTTCCAGATGTAGGTGCTCAATCTAGCAGCTTATCT
EST16904	7	C	T	---	---	ACAGACTATCGCCAACTTAAATGCTTAAACTTTATGATTCATTAAGTAAATAATAC/CJTGGATA TTCACACTTATTTAAATAAGGTTTGTGAAGATGATTTTCCAACTGTAGGTAAACAT
EST21863	49	A	G	---	---	TTTTAAGTACCAGGAGGCTGCTGGAACAGGATGAAACTGAAACTACACAC/CJGTACTACTTACTC TTCACCTCTCAAACTGATCCCTAAAGACTTCTACTTAGCAA
EST21885	80	G	A	---	---	GGCTGTAAGTAGAATCAAGGTTAAGAACATTTTATGCACTTATTTCCACAACAACTTACTGAGCATA CTAGGTGCTGGGAG/CJGTGACAGTGGAGCAAAAACACAA
EST22623	26	A	G	---	---	ATTTTAGTGCMAATGACAAAGCCCA/CJGAGAACAGAGGATCAAAATGAATTTGAAATGATTAACC TTCATAAGTATACGAAGTTTAAACAAAGTATGGGAGT
EST22644	98	A	G	---	---	AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACTGTTTAAACAGCACTAAAAATAA AAATTTAAATGATTAATCCATTTTACAG/CJAAATGTGGAAGAGATGGCTTTTAAACCC
EST23587	31	T	A	---	---	CCTCATTTATTTAAAAGCGGACATAAAAT/CJATATACAAACAAAAACCCCAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAATATGGTGG
EST24246	106	T	C	---	---	AAAGATCTGGCAATTTACATCACTTAAATATTTTGAATTAATCTTTTCCATGAGTATTTTTTCA TGTCCAAGCATTTAACTATCATTTTAGCGT/AAATACQ/CJGAAATACCCATAGTTACAGAATGG
EST24308	45	A	G	---	---	GTCTGTGAACCTCAAT TAGTTAAATTTCTGAACCTTTGGCTTTATAAATTTTCTCAACTT/CJG/CATTTAAAAATGATCAAT GCACCTCTCTGAGTAGTACACATGAAATATAAACCTCGTTC
EST24435	73	G	A	---	---	CTTGACTTCGCTTCAAGGTAGCTCGCTCAACCTCCCAAAATGATGCGATTACAGGCAATAG CAGCC/CJATGCTCGCCTGACCAATTTCTTTATCCGATCTGTGATGACATTCAGGTGTTTC
EST25089	25	T	C	---	---	TATTTGCAATTATCAAAATGGTTAT/CJAGTTTTCAAATTTAAAACTGTAATGATTTCTATGTATAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGTTAGTTAATGCTACAT

EST33508	36 A G	AAAAATGCTATTTGAACAACTTTTATAAGAG/GTAAAGTTGACTGAAAGCAGTTTAAAT
1a			AACATCAACTCACAATGACTTTTAGAGCCAAATAA
EST33863	77 C T	ACAACATAGGACTGGTTATTTCTGGTTTGAAATAATATGTTGCCACTTCTATTTGTTTAAATGA
4			TCATTTAAQC/TTCTTTGAACACTACAGCCTGAATCCCC
EST34739	97 T A	GAAATATCCTCCAGTGGCAGGAACCTGAAAGACTCCAGATCAACACAGGTGGACCTTTTGGTTGATGA
3			GCTGATAGCTTCTAGGCTGTGGGGAACCTG/AGGTGCTTACAACCTCAACTACTGACAGAAATTTCT
			TGTTGTCCTCATAAACA
EST34792	104 A G	ACCTGACTGCTTTAAAGCTCTTTGAAGCTGACCGTAGCAGACATCACGTGGCATCCACTATCAATA
6b			CTCATAGTCTAATTTATCCTCAGGATGTTCCCTGA/GGTATTCAGGAATTCCTTAGTCTCTATTACA
EST34835	93 T G	AAGATTTGTTGCTGTG
9b			GGAAATGTTCCCTTTGCAACCAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG
EST34835	82 G A	TGGGGAGTCTATGTTGCTTTCTGGT/GGGCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
9a			GGAAATGTTCCCTTTGCAACCAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG
EST35230	93 G T	TGGGGAGTCTATGTTG/ATGCTTTCTGGTGGCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
0			CACAAAGTCCACTTTACTTACATGAAGGAACATAAGGCAATGAGAAACAGTCAATCAATAATG
			CAAGACATGAGCATAAAAGAGTTCTG/GTGGCTTTCCAGCGTTGTTATACAGAGAGAAACCT
EST35337	33 C T	TCCTTTCAAAATTTTGATGAGGCATTTAATG/C/TTATAAATTTCTGCTTAGGAATGTATCTGCT
9			ATATCTCAGAAAGTTGGGCAATGTTGTTTCCATTTTACTTAGTTTCAAGCTTTTCAATTTTTCATCT
EST35708	32 C T	CTGCCCCAAATTAACTTTGGCAATGGAAC/C/TAGACTTACTGTATGGGACATTTTAAAG
9			ACAGCTTAGTAATAATGTTTCATATGACGCGTGTGCTTCCCTCTGAGGTTGSCACCTTTCTGTTGTG
			ATGTGCAAAAGTTGGCT
EST35747	51 C G	ATCCAGTCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA/C/GATGTTAAACGT
9			TTCCCAACATCAACCTAATACAGTAGACAGCAACACCTCCCTCTGAGGTTGAGATT
			G
EST35751	89 C A	TGGTCCATTATATTAACACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA
9			AGTTCTCCCATGAACCAAG/C/ACTTGTCTCATGATAAAGTGGAGACATAAGAAAGCCAGGT
			ATATAATTAAGGCCCTGTGA
EST36301	93 C T	CACCTGTTCTGTTGCTACTGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTCAGCTACAGC
4			AGTCAGGAGGCGCATGCCCTG/C/TGCTGATGGAGCTTGTAAATTTAGCCCCAAACATGATCTTCA
			GAAAGAGGTACAAACA
EST36519	33 G T	GCCATCAGCCCCACAAAGACATGACTACCAAGC/G/TTGGCCCCCTTGACCCCATACTGGCCTCAGCAC
0a			CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTCTGT
			CACAGGGTCTTAGTGT

EST36620	50 GA	---	GAC TTATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGGGAGJGCTAGGGTTTAAAGG
6			AAGGCCTATTATTAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690			CCTGTGATGTGCATGGTGCCTGAGCAGTGTACTTACTATGCGTACAGAGCTCACGTATGTCACGA
0a	89 CG	---	AAGGAAGTCTGGGGATTCTCTA/C/GJAGGGGACATATCACACATATCTTAAGTCACTGTGTGACTCGG
EST36729			CTTGAGCAAGTCATTCTCA
9	62 CT	---	GAGACAGGCAATCAGTTAAATGAGGTAGGCTCTCCTCTAATATATCATGATTGACAAATG(C/TJ
EST36823			TATTTAGCCAGGTATGCACTTTAGCTACCCCTGGACAACTGCTATCAAGTGTGCTGGGAAGGGAG
6	103 AT	---	ACTGTCTGCCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG
EST36987			GTCAGTATCTCGGGGTGCTATTCAAGCAACAATTJATJCTTTTATGTTCTTAAGCTCATCATGAG
4	126 CG	---	TTAA
EST37054			ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAAATGGGAGATACCCACAGACCTGTAAATATT
3	88 TC	---	TAAATAATATTTAACAGCTGATCAGAGGCTAAATTTACAACTGACATTTTGATGCACTTTJG/GJTTA
EST37269			GGGAATTAGACAATGAG
3b	105 TG	---	GGTCACTCTCTTGCCAGGACGGTGTGAAACTCCTGAGCTCAAGTGACCCCTCCCACTTGGCTTCC
EST37284			GAAAGTGTAGGATTACAGGT/CJGTGAGCCACACACCTCGGTCTTGTTTAAAGTAACCACTGAA
2	93 GT	---	C
EST37315			AATAGTCTATGGCTACGGGCCCTGGGATGTTAAAAATTTGGATTTTAAATTAAGATTGTGAACATG
2a	90 AG	---	CAAACCCAGCAATTTCTCAGCTATATTTTGAAGTCT/CJGAGGAGAAAAATTTGGGGTCC
EST37374			AAAGACCTTTCCACAGTAACTTTGAGCAGAGACTCAGATGAAGTAAAGGATGAACCCAGGAA
1	45 CT	---	CGCTCTGGATAATGTCACTCTAGGAA/GJAGTAAACAGGTGTTAAAAACCCCTGAGATAGCAACCT
EST37376			CTTGGCTGCTGAGGAATA
8b	101 GC	---	AGATGGGTCTGCTAGCTTCTCGGGCTGAACTAAGATATCTCTCTGCTCAGCCCTCCCAAGGTAGT
EST37376			TGGAACTATAGTAGGAGTATCTJAGJCCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA
			CCCCAGAGGACAGGACAA
			CCTGCCATGATAATGTTAAACATATCAAGATCTCCTCAAACTT/CJJAAGGGTGAAGAGCATACCC
			ATTCATTTTATTGTTGAAATATCTTCACATAGCCAAACACATTTTTTCAAGGCACCTCTAGCTACTACA
			GGA
			GTGACATCATGTCTCTCAATGCCCTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT
			CTCTGGTTCAATCAGAGTCTGTGCTCGA/GJGCTGCTCCTCAGGCAAGTTGTGACTTCTCTG
			TGTCAGG
			GTGACATCATGTCTCTCAATGCCCTTTCATTAATAGTAGT/CJTGAGCGCTGGGGCTGAAGTCAG
			ACTCTCTGGTTCAATCAGAGTCTGTGCTCGAGGCTGTCCCTCAGGCAAGTTGTGACTTCTCTGT
			GTCCAGG
			GTCTCTGGTTCAATCAGAGTCTGTGCTCGAGGCTGTCCCTCAGGCAAGTTGTGACTTCTCTGT
			GTCCAGG

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EST51340	51 GA	---	---	GATCAAACTGTATTGCCAGGCCAGCTCTGGAAGAACTGTGAACATAGAAGTGAACCTGAGCTCAGGCTAGAGGATAATGTGACCTCAATTTGCACACCATTGCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGCCCAAGGATTATT
J04162	134 TC	---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTCGAACCCCATCATCTCTCAGGCCCTCTACAAGCAGCAGGAAACATAGAAGCTAGAGCCAGATCCTTTATCCAACTCTCGA TCCTTTTCTTGCTGCTCAGTGGAAAGGGAAGCCCATGATCTTCAGCAGGGAAGCCCCAGTGGT AGCTG
K01506	63 TC	---	---	CTGAAGTCCAGCTGCCCTACAAAGTCCATCTCAAGCTTTTCTCTCACTTCATGTGAAAACCTAQT/CJC CAGTGGCTGACTGAATTTGTCAGCCCTCAAGCTCTGCTCTTATCCATTACCTCAAGCAGTCAATCCT TAGTAAAGTTTCCAAACAATAGAAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCCTTTTC ATTGAGCCTTTTATCCT
L18877	69 TC	---	---	TGAGTCTGAGCAGCAGTTGAGCCAGGCCAGTGGAGGAGTCTGGGCGAGTGCACCTTCCAAAGGCG CT/CJATCCATTAGTTTCCAGTGCCTGTGTGACATGAGGCCCATCTTTCATCTCTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTCTGTTCTATTGGATGACTTTGAGATTATCTTTTCTGTTCTGTGGGA ATTGTTCAAAGTIT
L31848	36 TC	---	---	GCTATTATACATATCCCAAGCCCTTAGGGCTACAGT/CJCTCTGTCCTGGACCCCTGTAGGGTGCCA TTTGAGTTTACAGAGCCTAGAAAGAAAGGCTTTGGGCTCTGGTGTGGCTAGGCTAGGCTGTAATCGT AGCGCTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 GC	---	---	GGGTCCAGAAGCCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGAGCTGGGCAACACCCAGCTCCGCCAC CC/GC/CJCTGCTGGTGTAGTCATAGAGCTGCAAGCTGGAGGTGGGCGATGGTGTGGTGGACCCCTCT CTCTAGAGACCTTGAG
L39059	123 TG	---	---	ACTTTGAAGGAGCAGCTGCCACCTCTCTGGAGGCCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGCAGACGGGCAACAAATACAGTAGTATTCTTTGTATTGTATATTTGJCGCCTGA AGATCATCCCGCAAGGCGAGGCTGGAGGTGGCGCTGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
L41264	173 GA	---	---	CAAAAGTTGCTCCTGCCCATGAGCACCAAGTCAAGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAAGTGGTTGCCAGCTCCAAATGTAACAGAGCTGGAACTTGAAGCGTGGAGTCTGCAT CTTAGGGCATCGCTCTTCTCTACACCAACAAATCTGAACATCTGACCTTCCCTTGCCTTACAAATGTCT AAGGT

U05641d	166	C T	---	---	---	CTCCTCTTTATTTCAGCATGGAGGGTTAAATGGAGGATCCTTTTCTCTGTGACAAAACATCTTTC ACAACTTACCTTTGTTAAGACAAATTTTAAAGATCTTTTACAACTTACCTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAGTC/TTTGAATTTATCTATGTCAATGATTTTAAAGCTA TGAATAATACAAATGGGGGA
U09607	39	T C	---	---	---	GAGGCCTTATGAGGGTCCTCTACTTCAGGAACACCCCAATTCGACATTTGCGGGGGCTCCCG TGCCCTGTAGAAATAGCCTGTGGCTTTGCAATTTGTTAAGTTCAAGACAGATGGGCATATGTTCAG TGGGGCTCTCTGAGTCTTGCCCAAGAAAGCAAGGAACCAAAATTAAGACTCTCGCATCTCCCAAC CCCTTA
U09608	82	T C	---	---	---	GAGCAGAAAGGCAAGCGGCAAGATGAGTTTGGGGTTGTATCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCCTTCACATCTGCCCGCCCTCCAGCCCTCCCGAGCCCTCTCTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	C G	---	---	---	GTGACATGAGGCCCATTTCTTCGCTCTGTGTTGAAGAGAGCAATCAGTCTCAGTGGCAGTGG GTGGAAGTGAGCAGCACTGTATGTCTCTCTGGGTCTCTGTCTATGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTTCAATGTCTTTTAAATGGTCAAGTTTAAATGAAGTTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C	---	---	---	AAAAGGACTCTGGTTCAATCCAGGTTCCATTTTGTATCTTTGTGACCTTGCACAAGTTGTTAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCAGAGAGGAACAGCCCAAGAGATTC/TTACCGTGGTCTTACTAAAGTACATATCCTTAACCTGG GGTTACCTTTCAGCA
U15555	187	T C	---	---	---	TTCTGTCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCAATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTATGAGTCCAGCAGCCCTTTTCTAAGCAGTCTGGTCCATGTTC/TTGGTCTCATAC CTCATATGCAGGATTCATTC
U17077	122	T C	---	---	---	TCCAATTTATGGTCCCAAGAGAGCTTCCAAAGTTTGCCATCTGGATGACAAACGGAGATCCACT AAAAGTCCACGGGATTAACAGAACGTCTTCGAGACTGCAGCTGACACACACACAC/TTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTCTGGGAAACAACTGCTCTCTGG AATTA
U18543	58	T C	---	---	---	GCACATGCAGAAATAGACTAGCCTATGCTCCTGATCCAGCTGGGTAGTTCTAGAAGTTTC/AGAAAG CTCCATCTTTATGTTTATTTGTTATGTCCCTTCCCGGCTTCCACCTTAAATTTAGAGCTTTAA AGATGCACCTGCCAAATAGGACACACAGTGGTGTAGCTGAAGTTTGAATAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A	<p>TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAGCCCTTTTAGTATATGAAAATTAAT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCAATACTGAATGAAGAGCAATGACTATCTCTG AAGACACCAAGAGAAAATTGCAAAAAGAC/AJAAGTATGACTTTTATGAACCCCTTCTTTAGG GTCAGAGGAATTTGGACTGA</p>
U25975a	143	C G	<p>TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAGCCCTTTTAGTATATGAAAATTAAT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCAATACTGAATGAAGAGCAATGACTATCTCTG AAGACAC/C/GJAAGAGAAAATTGCAAAAAGACAAATGACTTTTATGAACCCCTTCTTTAGG GTCAGAGGAATTTGGACTGA</p>
U25997	61	A G	<p>CAGGAGAGGTTATTCAACCTCACAACTAGTATCATTTTAGGGGTGTGACACACCA/A/GJTT TTGAGTGTACTGTGCGTGGTTGATTTTAAAGTAGTCTTATTTCTATCCCTTAAAGAAAAT GCATGAACCTAGGCTTCTGTAATCAATATCCCAACATCTGCAATGGCAGCATTCACCAACAAAA TCC</p>
U28413	29	C T	<p>ATTCTGACAGCTAAATTAGCCCTAAATG/C/JGGGTAATAATTTTCCCTCATGTTTTAAATGAGGT AATATTGCATAAATCCTAAACAGACTCTGTATAGTTTATTAGTCAAAATGTGTTCTTGATCC CAGATGTTGGCCTGGGAAAGCCCTCATTTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G</p>
U30884c	89	A G	<p>TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATCCACGTAGCC/A/GJTTGCTTGATGAATCTATATGATGATAGAACACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACITGCCACACAGTTGAACACAAAT GCTGTCA</p>
U30884a	34	A G	<p>TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTAGCCAAATGTTCTTGATGAATCTATATGATGATAGAACACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACITGCCACACAGTTGAACACAAAT GCTGTCA</p>
U31216b	78	A G	<p>GGGACAGCATATGTGGACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTATCA/A/GJCCCTCACTAAAGTTACCAAGGCTCTGCAAGAGCCCTGACCTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCGATTCGCTTTAGCCCGGC TGGTAGCCCTTCCAT</p>
U31216a	70	G A	<p>GGGACAGCATATGTGGACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCTGCAACCAACA GCC/G/JTCAACCCCTCACTAAAGTTACCAAGGCTCTGCAAGAGCCCTGACCTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCGATTCGCTTTAGCCCGGC TGGTAGCCCTTCCAT</p>

X54741	24	A G	---			CAGGCCACCTGCTCTCTCCACAGTGACAGCTTCTGAGTCAACCCCTCTGTCAGCCAGCTCCT GCACAAATGGAACTCCCAAGGCTCCAGGACTGGGCTTGGCAGGCTTGTCAAAATAGCAAGGCAG GGCAGCTGGAGACGATCTTGCTGGCAGGCGCTGGCTTGTCCCGAGGCCACCTGGCCCCCTCTCC AGCAAGCAGTGC
X54869	99	A G	---			AAGCATTTGCGTTACAGTGCATCAGATACATTTTATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATTATTTGCTCTAGATACAAAATTTCTAAATCAATTTATTTGAAATAG GATGCACAAATTAATAAGTACAGACATCTAGCATTTGTGCGGCTCATTTTGTCTCAACATGGTA
X66924	147	G A	---			GCGGTGCTGACACCTCCAGAACGCGAGTGTGGGCGCGCTTCTGGCTGGGACCCCGGGGAACCTCTC CTGCGGGAAGCCGACGGGATGGGCGCAACTTGGCGCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTG/AJACCTGGTGTGCTCAGGCGGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA
X78932	62	T G	---			GAAATGTGAAGATGTGACAAAGCCTTTAAGCGGTGTGCACACTTGTATGTATATAAGATAAT/GJT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAGCATTTATCTTGAAGAAAATTTGTATAAGAAATGGAAAAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25	T C	---			CTCAACCCATAACCTCAACACATCTGTATCTCCACCCACATCCACACATCCACCTCCATCC CCAAACCATCTCTATCCCACTACAGCCCAACCCAGCCCGCCAGACTAATCCACAGCCATCCCAA CTCATCTCATCCCACTGACAGCCCAACCCCAACCCAGGCGCATCCCAACCCATCCCAAGGC AACTCAACACCATCC
X80197b	99	G C	---			ACCCAACTCAAGTCCCAAGGCCCGGAGATCTTCTGCGCTGCTTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTGCTAGCTACTTCTCTG/CJCACTTTGAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCACTTCTGGCTCTGCCACCCCAAGTGGGAAAGGCCACCCCTAGAAAG
X80197a	28	A G	---			ACCCAACTCAAGTCCCAAGGCCCGGAGTCTTCTGCGCTGCTTGGCCCATCCAGTCCAGTCC AGCGCTGGAGCAAGTGTGCTAGCTACTTCTCTGCACTTTGAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCACTTCTGGCTCTGCCACCCCAAGTGGGAAAGGCCACCCCTAGAAAG
X85106	150	G A	---			GGCACCCAGAGTGAACACAGTCCAGCAGGAGCGGCGCGCTCGCGCTGTGCTGTTCTTTT CAGCCCGGAGAGGTCTGAOCTGGGGCTCTCCAGGCTCTCCAGGCTCTGCGCCACGCTCCCGCGCTCT CTTTCTCCCAAGC/GAJAAACCAATGCGGCCCTTCACTCTGCGCGCTGCGAGGCGGGGCTT CTTTCAAGC
X87160	128	T G	---			ACCCAGCCATGGTGTAGGACATGATGGGTGCGCCCAAGAGCTGTGCACAGGGACCCCTCGCC CACTCTGGGCTTTGAGATCTGACCAAAAGGCTGCTTTAAACCGCAAGATGGGCGCT/GJGGC ATGCGCAGGAGGCCCTCGGGTACTACGCAACACTCAACACTGTCCAGGCTGAGATAATCCC GGGA

1282	130 C T	---	GTGGATCACCACCTACAGTCTAATTTTCAGATGTTTTCATTACCCCTAAAGAAATCTTGATCCCATTA GCAATTAATTCCTCAATCTGCGCTACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCCQCTACT TGACATATCATACACATGGAGCCATACATATGTGCGCCCTCATGATGGCTCTTTCACCTGAGAATA ATGTTTCAAGGT
6810	68 C T	---	AGTATCACACATACCTTAATATATAGATATACACAATAATAAATCACTCCCTACCTTGAAACCTTT A/C/TJAGAAGCATTTTAAATTTTACAAACAAGCTCAACGAACCTACAATAAGCTAGTAGCTG TTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCTTTTAAATGTCTATGAACAAGTACAA TTTCTTTTGTGTTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118 A C	---	CCAAGTACATTTGGTGAACGATGAGCTAGCTGTCTAGTATTTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAAACATCATCACTAACAATGTAGCTGCAGGTAACJACJTGTTGGATACCCCTG TGTGCTCTACTGGCTCCAAAGGCATTCAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAAATC TTGGTTCAAGTGGCGCTGTGCAGATCGGCTTTTGGTTGGTGTCTAG
6819b	212 C	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGTTGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAA CAGCAATAACCTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGTTGGTCTTCAACAGTTTGTG/CATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39 A G	---	CTGGTATGTCATAAGCAATCCATAATTTGTATAGCTATTTGTTATCTATGGCACCATTGCGGACA CAGATTATATGTGACAGACCCAGCAATGTCCTTTAAGATATGCGAGCAACCAAAATCTGTCATGGT TTAACAAGAAATGAACGCTAGG
6972b	149 G T	---	AGGATCCCTCTTTTCTATGATTGAATAGTTTCAGAAGGAATGGTACAGTTCCCTCTGTACCT CTGTAGAAATTCGGCTGTGAATCCATCTGGCTCGACTCTTTTGGTTGGTAACTATGATTATGCG CACAATTTCAAG/GTCTGTTATGGTCTATTCAGAGATTCAACTTCTTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G	---	AGGATCCCTCTTTTCTATGATTGAATAGTTTCAGAAGGAATGGTACAGTTCCCTCTGTACCT CTGTAGAAATTCGGCTGTGAATCCATCTGGCTCGACTCTTTTGGTTGGTAACTATGATTATGATT TTGCCACAATTTCAAGCCCTGTTATGGTCTATTCAGAGATTCAACTTCTTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CAATGCA[AT/GA]
7598i	192 G T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598g	142 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598l	120 A G	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598e	83 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598d	77 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATATGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCT CCTCAATGCAGA

WI-18562	29 GA ...	---	CTAAGGAAAAATTAATGATGGAATATC(G/A)ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTTATTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAAATGATCTTACATT TAGCATTAATCAGAAACGA
WI-18618	51 AC ...	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC(A/C)CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCCAAAGTATAAATGTTAAACCCACAGTGCCTGCACAGTTC AC
WI-18683	22 CT ...	---	TAAGCTGTTGAGGACTGACTC/TGGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCAAAGCCTGCCCTGAGT
WI-18520	75 GA ...	---	GACTTGGTGAATTAATGCTTTCCCTTAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACAG(A/C)CCGGAGTGGTAAATACTACTACTACTGCAACAAACACGGGCATCCACTGCTCTCAA TGCTCTTCCTGAGAC
WI-18563	94 AG ...	---	AAATAAAGTTTATTGGCACAGCCAGCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAG(A/G)GACATGGTGTGGCTCACAAAGCCAAAGATATT GTCCTATTCAATTTAGCTAGAACCAATTTCTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC
WI-18562b	69 TA ...	---	TT(A/G)TGCCATAATTTATTATCAGTGCCTAATTTGAAAGACATTTGGATCGTTTCCAG AACTTTATTGATCTGACGATCAGGATAGTTTCTCATCCACATTTGACTGCTGTAGATTTTGAAG TGTTAACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723i	94 GA ...	---	AACTTTATTGATCTGACGATCAGGATAGTTTCTCATCCACATTTGACTGCTGTAGATTTTGAAG TGGT(C/A)ACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 TC ...	---	AACTTTATTGATCTGACGATCAGGATAGTTTCTCATCCACATTTGACTGCTGTAGATTTTGAAG TGGTAAACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ...	---	TTTATTACAATATTAGTGGCACAAATAAAGCTTCTGA(G/A)ACAGGAGGTAAACATCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18619	44 GA ...	---	TTATCAGAAAAAGTGATATTGACAGAGGTCTGGGGCTGTACATGGCAGGGCTGGTGGAGCTTTG TACATGGG(A/C)CTGGGAGACAGGAGCCCTCCAGGTGGAAGGTAATTTTTTAAATAAAAAATAA TGGAGCTACACACACCCCTG
WI-18715	76 GA ...	---	GTAATAAAGTTTATTGGCACAGCCAGGCTTATTCATTCATATGCCATTGACATGCTGTGGCCT ACACAGCAGGTTGGGACCTGCTCTTCCAGGGAGAGCTA(G/A)TTGTTTAAAGCAGTGGTCCCAAC CTCTGTGGTCCCTGGT
WI-18535	107 GA ...	---	AGAGTGGTCAAGACACAGCCGCAATCCAGGCTTATCAGTTACTAGTTTTCAGTTCTGGGCAAGTGAC TTTCATCTCTTCGAACCTTCAGTTTCTTCATAGATGGAA(A/C)TGCTATACCTTACCTACCTGTA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAAACAGTGATACATACACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTCTACCAAGCCAGACGAAG
D17525	107 CT ...	---	

DWU-133c	313 A G	TAA TTGGCCACTGCCTTATTATTACAAACAGAAATGTCTCATGACCTTTTATGTGTGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACAGACAGAAATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAAGTTTGTGAATTTTAAATAGTAACCTC AATTCAGTAAATGGTATACACTGCTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C	TAA TTGGCCACTGCCTTATTATTACAAACAGAAATGTCTCATGACCTTTTATGTGTGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACAGACAGAAATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAAGTTTGTGAATTTTAAATAGTAACCTC AATTCAGTAAATGGTATACACTGCTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T	TAA TTGGCCACTGCCTTATTATTACAAACAGAAATGTCTCATGACCTTTTATGTGTGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACAGACAGAAATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAAGTTTGTGAATTTTAAATAGTAACCTC AATTCAGTAAATGGTATACACTGCTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T	ATGAGATCCTTTAAATCCTTCATGAAAGCTTTTGTGGTGGCCACTCTACGTCAACATGAAGTG TGTTCTTCAGTGCATCTGGGAAGATTTCTACCTCTGACCAACAGTCTCTTCCAGCTTCCATTTGCGC CCTCATTTATCCCTCAACCCAGCCAGCCAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTCTATGTGGAATATAAAGAT
DWU-387	169 G T	GTGTATAAATGCAACTGTGATTCTCAACATGGCTCACAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTGTGTTTAAACTGCACTGCCAACAAGTTCACCTCATATATAAAGCATATTTTAA CTCTTTTGAGGTGAATATAATTTATATTACATG/GTAAAGCTTCTTAACTACTAAGTATTTTCA GGTCTCACCAGTATCAAGTAAATACACAAATGAAGTGTCAATTAITCAA
DWU-447b	172	ATTTAGTGTCTTGGCTTAAATAATCATTTGAAAAGTATTTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGTGTTGCCATTTAAATCACTGTGAATTAATAGTTTGTATAGACACAAAGCTTAGCTAATCAA CCATTTTTCATTTTGTGTTCTAGAGGATTGANAATCAGTTTAAATGTCTTCTTCTGTTAG GCCTTTCTTCTTACAAATGAAGAGATGATTTCTTAGTTTATGGTTA
DWU-447	85 A G	ATTTAGTGTCTTGGCTTAAATAATCATTTGAAAAGTATTTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGTGTTGCCATTTAAATCACTGTGAATTAATAGTTTGTATAGACACAAAGCTTAGCTAATCAA CAACCATATTTTCTTGTGTTCTAGAGGATTGANAATCAGTTTAAATGTCTTCTTCTGTTAG TTAGGCTTCTTCTTCAATGAAGAGATGATTTCTTAGTTTATGGTTA
DWU-476	63 C G	GTAAATTCAGTTTCTTCCAGTCTCTTTTGTGCTCTCTCAATAGCGTTTAAAGGTGAGTGTGAT AAATCAACTGCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTCTGGGAGATTTTTT

DWU-505	67	A	---	---	TCATCTAGGGCAGTATCTCCTCTAGCTAGTGCCTACACAGAAAATCTATCACCATACAAAATTTA A/TTCAGTATTATGTTTAAAGCACACAGGTGTACCGAAACTGTGAAAGTCTGAAATTTATGGGT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGGACTTTGAGCTTTAAACTTTTAA
DWU-512	131	A	G	---	AAAATCCAGGCAATTCGAATCTGTTTTTCATGATTATAGAGGGTTTACACAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAAGGTGAACCTTGCTTTGAATATCCAGATGTGTTTGGTGAAG TGCGTATGGCAGTGAGCAGGTATGTTGCTTTTCTTGCTTGCACTGAAATTTAAATTTGCTATCAAGAGC AAATATGAACGGTTTTTTTATCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A	C	---	AACTGCATATAGATAATATCCAGGATGTGGCTCATTCTTTTCAGCTTGTTTCTTACTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTAAAAAATAACATATCTTCTGCTTCAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTCG
DWU-59	94	C	T	---	CATTTCTTTGTGAAGGTAAATGGACTCAAGAGGGGAAGAAACATGCTGAGAAATGAAAGTCTACCGG CCCTTTCTTTGTGAACGTCAATTTGGC/CJTGAGCCGTGTTCCAGGTGCGAGTCCAGACTCGTTTGTG GTAGTTTGTTTTAACTTCCAGGTGGTTTTTAACTCTGATAGCCGGTGAATTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C	---	---	CTTGATCATGGGTGGAAATTTTGTGATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63	C	T	---	CACACTGCGATCTAGGCTTTGGCTTGCAATTCAGAGGAGAGAGCCAGTCCCTCTCTGGAGA/CJTG CTGGTTCCCGAGCCCGACACCGGCTTTGCACACACAGGCTGTTGAGCAGGAGTGGGTAAGACGT AGCTGTAGACCCCAAGCAACACCGCCCTGGGACCTTGCGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGTGGTCTATCCCATCTAGACAAGACACATCTACATAATAAAAGT
WI-18014	40	A	G	---	TCCAATTTACATTTGGTGGCAATTTGTTGAATAGCTACAGAA/CJGAAATGAAAGTGCACCATCAGAGT GTAATAGGCTGTGTGAACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97	T	A	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCAGAGTGGAAATTTTAACTTCTTATAA/CJTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGATCTGAAGG
WI-18036a	27	T	C	---	TTCCAATGTAAGAGTCAAGTACCAAGTT/CJAAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCAGAGTGGAAATTTTAACTTCTTATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGATCTGAAGG
WI-18046	72	C	T	---	TGTAAGGTGACTTCTATAAGTCTTCAACTGCAACTTTCATTACTGAGATTATTCAGGCCAAT GTGTC/TJTGTTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAAACCTGTTCTCTGTTTCA

WI-18063	105	G A	---	---	AGGCTTTAACTGATAACAAATTTGCCCTTAAACACATACAAAACTCTGCACCTTCCTTCCTTC
WI-18078	86	A T	---	---	CCATGTTTCTGATTTTGATGTAACCTTAAATTTGJGJATCCTTTAAACAATATACTAGCTGCA
WI-18091	90	T C	---	---	AGTTGAAAGATCAGAGAGGTATGGTTGGTGAGTAGCTGAACCTCAGATTCAAACCTGGTCCAGTGTG
WI-18119	38	T C	---	---	TTGTTTTTTCAGCATCAGATGTCACACTAGCCAAAGTTGATCTCTCGAGTATCTACATGTGGT
WI-18142	66	T G	---	---	CCAAAGCTCACTCAGTATTAACTATCTGCTAAATTCATCCTTTGTTAAATCCATCAGACACTGTGGT
WI-18178	68	T C	---	---	TTTCATCTCTAGAAGTTTGACTTTCJGGGCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18244	35	G T	---	---	GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGATTCJTTGTAATAATGGATTGGAGTACTTAC
WI-18245	115	G A	---	---	CACTATTCACTCTGCTCTGAAATAGTTCACTAACCAACTACTGACAAACAGTTTAAATTTGGTTCTT
WI-18261	26	G A	---	---	TTCAAGATAATTACAATTGGAAGGGACCAATAATCCACATTTTAAATCGAAAAATAATCTATATACJ
WI-18268	88	C T	---	---	TGJCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18299f	107	C A	---	---	GCATAGGGTTGAGGGGTGTACAAAGAGGAGAACAGATTCACTGCTGATGCTGCGTGGAGGTAGTCTGGGG
WI-18299e	101	A G	---	---	GTTCJGGCGGGATGACACACAGACACACATAGATCTGGCATCTGATAGCAGGCGCATACAG
WI-18299d	77	G A	---	---	TCAATCTGAAAACTTTGCTGTAGCCAGCATGGGGTGJGJGGGAGGTGATTATGCGCTGGGGAAGATG
WI-18299c	67	T G	---	---	GGCACTACCCGACACAGCATCTAGCAACACAGTGACAGGGACGTTGAGGTGGCAGAGGGGCTTT
					ACAGATGTCAGTTGTTGAATTGGCCCATTAAGATATGGGGCTTTCTTGTAAAAAGTCAATCCAAA
					AGGCTTGGCAAGAGTTTGTCTATACAAACGGGAGGACAGAGAAACATGA/GA/CTGGGAGTAGGCTCT
					GACAGAAGGTGGGCTGTC
					GATTTGAAGGGATTGCTTTATTAACTGATGAAAGCGTGTATAGAGGAACGTGTTAAGATAAACAA
					CTTATAAATACTCCCAATTTGTAGAAGTGAAGATTG
					TAGGAGGGAAGAGGAGGTGGGCTGCTGGGCGCTCAAGACATGAGAAAGGGGTGGTGGCTCCAAAGC
					TTCCCTTACTTCCCGCATAGATCTCTGACATGTGCTGCAGAAAGCCCTCCAACTGGAAAC
					TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGGCCAAATTTTT
					ATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAATTTTGAAGAATTTTGGCCAAATTTGACATATCTG
					CAG
					TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGGCCAAATTTTT
					ATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAATTTTGGCCAAATTTGACATATCTG
					CAG
					TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGGCCAAATTTTT
					ATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAATTTTGGCCAAATTTGACATATCTG
					CAG
					TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGGCCAAATTTTT
					TGJATCTATTGGGCTGAGAAATCCACAAATTTGAAGAATTTTGGCCAAATTTGACATATCTG
					CAG

EST5	93 A ---	---	CTGTGGGAGGAAACAAATTTGGTATATTCATCAATGTAAGAACTCTTCAGAAATAAGAAAGAA CAAACCACTGAATCACACACATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTCAGAAATTTGAAGAGAAATGCAATTTGTGACTGAACCCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTCTTTTGCACACAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A ---	---	GGACAGGACCTCTATTCGCGCTGGTGCCAGCAGCGCTGATGACTGAGGCCCCAGGGACTACTGGGCG CTCTCTCAGGGGCTCTCCAGAACCCAGAGCTGTTCTCTGAGTTTCCCTAGAGCTGTGGGCGCA GATAGCTGTTCCTGAGTTGCAAGCACGATGGAGATTGGACACTGTGCTTTTGGTGGGT
WI- 18740c	104 GT ---	---	TCCTCATTGTGGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATCCAGTAGTG/TAATAATCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---	---	TCCTCATTGTGGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 CT ---	---	CCAAAGCTCTCTGTCGCTATAAGAAATTTTGGGATGGGAGAGAAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTCATTTTACAGAGGTAGCACAA/C/TJGATTCCAACACAAAACCCCTTCCOC TTTTAAATGATTCTGTCTAATGCCATAGATCAAAGGCCCTCAGAAACCATTTGTGTGTTTCCCTCTT TGAAGCAATGACAAGCACTTTACTTTACGGTGGTTTTGTTTTCTTAT
WI-18746	114 GA ---	---	GCCAGCAGCTGAAGTCTCTTTTCTCTCTCTGGCTGGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTGACTTGAACCGTTTTATATTACTTTTGTAAATATTTTJG/ATCCACATTTCTACTTCAGCT TTGGATGGTTACCG
WI-19112	212 GA ---	---	CCGTGTCACACACACAAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATGATGCTATCTCATGACAAACCCACAAAGAACCCGACGACAAA TCTTTTGGGAGATTTTCTCTAGTGGCTTGAACACATGGCTTTAAGAACACCGGTATATCTTTGAG GGTGACAAGGG/G/ATCTCTTCAACAGTTCCATACCAACTGCTTTCCTCTAG
WI-19092	232 AC ---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCCTCTATAAGAGGCTATCTTAGATCATGT CTCAATGGAAACACTCTCTCTTCTAGCTTACTTGAATCTGCTCTAATAAGAGTAGAGCAACACAC ATTGAAGCTCTGATCAACGGCTCGAAATTTTCTCTTGAATGTCTTTTAACTGAATTTTC TTTTAAGCTAACAAAGATCATATTTT/CAC/ATGATTAGCCGTGTAACT
WI-19057i	175 GA ---	---	CCCATTTTATTAGGCCAGTGTCTCAAGAGTAGAGGCGCTACTGTCTTTCACTCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTTGACGCCAGGACCCGACGACCTG TCTTCATGCGAGGAACACAGTGCCAGATCCCAACAGCTG/G/ATCTCTTCTATCTTTGTTTGGCCACA

WI-20103	168	C T	---	---	TGGGACTTCCAACTCAGAGGATGTGGGAATCCACGTCAATGATACAGATAAAGTGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGGAAGCTGGGTCTCCCAACCTTTCATCTGCTCAAGCTCTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCTAGCCTATCTTCAGTCAACTGGGA
WI-20441	111	G A	---	---	GCCTTACCCATTTTGCACATATACATATGACCCCTTTCAGTGGCAACATATATCCACACTA TAAACATACCACATTTATAATCTGTAGGACACAGAAATGGAJTTGAATAAGTACCCCCAA CATATACAGAAAGTTAGCATACTTACCCCGTTTTCACATCATCAGGGCAAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G	---	---	TGGTTACAAAACCTAAGCCATATACAAAATAGGAACACATTTAGATGCCCTCTTTGAAAGAACGT TTTAGTCTTTTAACTGAGTTTAAAAAATAACAATGCAATTTTAAJGJACACTGTTTGA ACTTAAAGTGCAGCAATA
WI-20813c	165	A G	---	---	GTCTCAAGGGGGAGAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGSCATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAJAGJAAAGGAGTTTCCACGCGCCAGTGGTGAGC
WI-20613b	156	A C	---	---	TGC GTCTCAAGGGGGAGAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGSCATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAJAGJAAAGGAGTTTCCACGCGCCAGTGGTGAGC
WI-19984	47	A G	---	---	TGC CAGTAAAGAGTGATTCAGTTCAGTAAATACACTGACAGGTAAATAJAGJTATACATTAGAAAA GCAAAATCTTTTAACTTAAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAAATACAGG TAGGCAAGAGTTTTCACACACTGGAAATGAAGGCGAGTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---	---	GCAGTTGGAATATGGCTATACGAAACCAAGAGTGTATACAAATGGAAGTGGTCATCAGGCAATA ATTGTTCTTCTTGGAACTCTGCACGAGCTGCCATGCTCTGTGGGAGCTTACACATCAAGTTTGACAG TCTGAAACCAACTGGAGCTCTTTCCAGAAATGTTCTGTTGCTCTTCAATAGGAATTCATG TTATTTCTTCTTGGCTTAAAGCTCTTATCTTCAATGACCTAAGCTGA
WI-18846a	49	G A	---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCTGJAAAGCTGGGAGCGT GGGCTCAGCAGGCTGGTCACTCCATCCGTAAGACCTCTCTCCCTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---	---	AGCAGTGGCCCTTATTCATCCCAACACGCTCTTGACCAGGCTGCTCTTGTGGCAGCAACGGC ACAGCTAATTCTACTACAGTGTCTTTAAGTAAAAATGGTCGAGAAAGGACCGJAGJGAAGCGG TCTGGGCGCTGGCAGTCCGTCGGGAGGAGTGGTCTGGCTGTTGAGATTCCTAAAGGAGCGAGCAT GTGCTGGACACACAGACTATTTTAGATTTTCTTTTGGCTTTTTCGAACC

WI-19067d	202 T G ---	---	TAATGCTGCTTGCTACGCTGACATTCAGGGCAGGCAAGGCTGCTCAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAAAT/ GACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19067c	153 G C ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19067b	151 T C ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19067a	57 C G ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-19106	247 T C ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-18944	147 A G ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-18952	232 G A ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC
WI-18932d	177 C T ---	---	TAATGCTGCTGTGACGTGCTGACATTCAGGCGAGGCAAGGCTGCTGAGGCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTCTCTC TTGGCTCTAGGCTCGTGGAGAAATGTTGAGGGGTTATTTTTTAATAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTTATC

WI-19042	193 A C ...	---	TTGTGAGTGTGCTCTGCAATGCTCAGTAGCATCTCAGTGGTGTGAAGTTTGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACTTTGTCTCAAGGACATTGGTGAGAGTCCACAG ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAATACTCTAACCAJAGJGGCTG TGTTAGATTGTAATACTATCTCTTGGACTTCTGAAGAGACCCTCAAT
WI-18984	208 A C ...	---	ATTGGCCCTGTACAGTTTGTCTTATTATTAATTCATTAACACTACAGGTGTTGAATGGTTAAAA TGAGCCCTCAGTTCATTTCAGTTATTTCTGAGTGCAGACAGCTATTTGCACTGTATTAAAT GTAACTTATTAATGAATCAGAAGCAGTAGACAGATGTTGGTCAATACAAAATTGTGATGCATT TATCTTACJATAAATGCTAAATGICAAITTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ...	---	GCTTCAATGGCGATTGATTCAGTGCCCAATTAACAGGGTTGGTAGTTTACTCACTATTTGAAT ATACCTTTTCTTATTTGTAATGTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ...	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGAGGGC ACAGAGGCTGCGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGAG GTGCTGTGT
WI-18821a	69 C T ...	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGAGGGC ACJTAGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGAG GTGCTGTGT
WI-19021a	20 C G ...	---	ACTCCTCTGCTGTGCTCCATGJAGTGTCTTTGAACCAAGAAAGTCACAGATTTAAAGAGAA GCAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAGTGTCTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGAGGTGGCATCTCTACTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGCTC
WI-18908	70 G C ...	---	TGGAATTCCTTCATCTGGAAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAAGGGTCACTA TGGJGCTTAGGGAAACATTCCATCCTTGAGTCAAAAATCTCAATCTTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ...	---	CACGGTCTCTGCATGTTACAGAGGGCTTCTGGTCTAGCCACGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTTGGGCTCAAGTCATGCCCGAATTTAGATGTGTTCTTTCTGAGAGGGGTC CCCTCCCTTACGAACACAJAGJAAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCGAGGCACTGGGGGTGAAGTGTGTTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ...	---	CACGGTCTCTGCATGTTACAGAGGGCTTCTGGTCTAGCCACGCCCTGTATGACCGGCAAA ATATCCCAAAGCTTTTGGGCTCAAGTCATGCCCGAATTTAGATGTGTTCTTTCTGAGAGGGG GTCCCTCCCTTACGAACACAAAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCGAGGCACTGGGGGTGAAGTGTGTTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ...	---	TTGAGGAGGTGGGTGAATGCTCTCTGCGAGGATTTTGACACTGCAATTTGCTGGGCTGTGTTCTQI/ CPGGGCTCTCTGAGACCTTGCAACGTTGATACAGGCCATGTGCCATGGTATTGGGCTCTGGAGGG TGGGTGAATAAAGGC

[illegible]

WI-19766b	93 A G ...	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGTGCAGCAGCATCCTTTCTGTGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCTGACAAACAGAAAGAGGACACCAAGCCTGAACCCCTC
WI-19766a	31 G A ...	---	CGGACACAGCAGAGTTACAGCTAGGGATGTCCTGTGGAGTTCTGACCCATGAGAGGCCCCCTCACCCCTCTCAACCTCTCTACCAACCAAGCTCTCCGCGAGTCATGGACTTAT
WI-20512d	126 C G ...	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGTGCAGCAGCATCCTTTCTGTGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCTGACAAACAGAAAGAGGACACCAAGCCTGAACCCCTC
WI-20512c	59 T G ...	---	CGGACACAGCAGAGTTACAGCTAGGGATGTCCTGTGGAGTTCTGACCCATGAGAGGCCCCCTCACCCCTCTCAACCTCTCTACCAACCAAGCTCTCCGCGAGTCATGGACTTAT
WI-19599	230 C G ...	---	CTTCCTCTGTTTGGCTTTCATTTGTGCGATTGTGCGATTGTGAAACACCATTTGAAAGAGGGACTTTCTGCAAACCTTAAAGACTGGTTAAATTACAGGCGCTAGGAAGTCACTGGAGCCCTTGACTGACGAAAGC
WI-20679	82 T C ...	---	TTAGAAAGGAACTGAAATTGCTTCTTTGAATATGATTTAGGCGCGGCGTGGGTGGGCTCACGCTTATTAATCCAGGCAAGTTGGGAGGGCCCAACGCGGGGTGGGATCACTGA
WI-19909a	29 T C ...	---	GGGCTTAAATTCCTCTGTTTGGGACTGGTCTCCAGTTTACAGCAAGGATCCACCCCTTTCCATAACCCCTTCTACATTGGAAGAGCAGCACCTTGTATACAGAATGGTCCGGAAGTCTTTTAAACG
WI-20341	221 G C ...	---	GACAAAGGTAAATCACAGCTAACAAACCGTGTGCTCACACGTAACCAACACCTCTTTTCA
			GAACAGAGAGCGTTAAAGTAAAGGCGACGTTTCCAGAGTAAACACTGCTA
			TGTTTGAATATAAATTTCCATGGTCTTAATTGAACCTGTATGTACTTTCTTTTGAATATCCTTTT
			TTCAATTAATAATTTCTTAAACCACTCTATGTGTTTCAACCTCTGTTTAACACTAAGATATGGGT
			TTTGGAAAGGCCAAGTCCACAGCTCCAGTGAAGTGGGCGAATGGTCTGTTTGGAAAGCTCTC
			CAGGCTGTTTCTCCAGAA
			CCAGAAATAAAGCTGAATCTCTTCTTC/CTTAAATAATAATTTTCTCTTTTCTTCTTCCAA
			GTAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGG
			TTTTTCTTTATACCTTGTCTGTACTGTGAATCAACTAA
			TTGAGAGCTGAGAGAGGCTGTGAGACATTGTAAGTCTTAGGGGCTGAGACATTAGGAAG
			GCCCAATTTAGTAAGTGAAGATGTGAGAGGCTGATGAGAACTACTGCTCCCATTTGTTAGCAGGA
			GGCAGGAAAGTATCTGGGCTCTCTGGCAGCAAAAGCGTGTGGTAAATAATTTGGGTGAGCTATGC
			ATCCCCCATGCATTTGGTTTTC/ATGCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60 T C ...	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATAGTGTC/GGA AACAGTAAAGCAAAATACACACAATTAGGAGGAATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAATCTATTCCATAACCAGGTAGATAATGTGACACA GCTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCGTATT
WI-20895	107 G C ...	---	TGATGGAAAGTACAAAGGCTCTGAAGAAGACAGAGTAACAGAGCGCAGTCGAGCGGTGGGC CACTCCACAGGAGCAACACTTGACTTTCATTAAAGGCAAG/GCTTTTACTCTGTACTTTTTCCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATCTCACACTACTGCTCTCTAAGGTCTTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ...	---	CCTGCAATCACAAAAGTGAAGTGAAGTGTGATATTTTGAATCATACTTGATTTAAACCACCTTCAGAAA TTCATATC/AAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ...	---	CTGGATTTTAAATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCAGAGATTCCTTAAGTAAGTATTGACGACTGAGACTAGTCGGCAAA GTCAATGAGACCTTAGCTGATCTCA/TAG/AGTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAAGTGTGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ...	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACTTCTG GGGTGATGATGAAGAGACTGTTGGTCAATGGCGGTGA/C/TGTCCTCTCCAGGCTCATATGATGTCT CGAGTTGCACAGGGAACTGCTCTGCTTGTAGAGCTTCTCC
WI-19348b	98 G A ...	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACTTCTG GGGTGATGATGAAGAGACTGTTGGTCAATGGCG/G/AGTGAAGTCTCTCCAGGCTCATATGATGTCT CGAGTTGCACAGGGAACTGCTCTGCTTGTAGAGCTTCTCC
WI-19635	98 A T ...	---	ATTAGTTCGTGTGGGCCACATTCAAAGCCATCCACAAAGCTTCTGTAGGCCATTGTAAACAAATG TTAAAGGTACAGTAAATAACAGTATTA/TATCTTATTGTGTAGCACCGGTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGCTGAAAGAACTTTGCTTT T
WI-19641a	46 A G ...	---	TCCAAATTTTCAGAAACATGTTCCATGTTTATGTGATAAGCACTAG/AGTATATAGTCTCATGTTT TTAAATTTGAATAACGTGTGATTCATTTGATTTTATTTACAGAGATGTCAGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGATAAGTGCATAATGTGGTTTAAATTTTAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACTTG
WI-19642b	52 C A ...	---	ATATAGTACCATCCATGTTTCAAGATGGCTGGACACATATCCCTTC/AGSGTAAACCCAG GACTATTCATGACATCTTTAATACGTATTTGATGGACACAAAGTTTCTGTCTATTA TCTGCCATGATCATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTCTGTGTCAITGSCCT TACTCTCAGTGAAGTGTGAGTGGATTACCTACCCCTGCTTTTGCATCCACTGTAATCTAATAGT GAAAGGCAATGATGCTCAGTATCATCTGTGAAACATTTTTC/CTTGGACCAAGCTGAAAGAA TCTTGAGGAGCCTGAAGCTTCAAGGTCCACACGTCAAAACACACAGCCC
WI-19673b	180 C T ...	---	

WI-19673a	35	G A	---	---	---	TCTGCCATGATCACATTGTGATGAAGAACATGATG(A)TCACTAGTAGGTAACCTTCTGTGTCATTCGCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCACCTGTAAATCTAATAGTGAAAGGCGAAATGATGTCTCAGTATCAGTGTGAAACATTTTCCCTTGGACCACTGAAGGAACTCTGAGGAGCCTGAAGGCTTCAAGGTCCACAGTCAAAAAACACAGCOC
WI-19724	35	A G	---	---	---	TTTATTGGGAAACAAAGGATTGTAAATTTGGGTAA(A)GCTGAGTCAACGCTGGCCCTGAGTAGTGTCCTAGAAACACAGAGATTGTGGTTTCTCTT
WI-19307	196	T C	---	---	---	TTCTCTCCCCAACTAGATGATGATTCATCATCTGCCCCACAAATGGTACCCCTTCAGCAAGAACTGCAAGCCCTCTGGATTTCCTTCATGAGAAATGGTGGTGGAGGTGACATTCCTTGTCTGGGTGAACCTGCAAGGAAAGGAAACCCAGGCAATGATTCATAGAGCCCTTAAAGAGACCCGTCGTGGAAATGGCCATGGTCTAATTTGGTGTGAAATTAACCTTCTTGGCTG
WI-19269	85	A T	---	---	---	CTTCCCTCATCCCTCTCCACACACCATCCCGGAACAGTCTCCAGGATTCCTGCCCCACTGGCCATTTTGGAGTGTCCJA(T)TTGGGTAGCAATGTGGAACACCCAGGGCCTTTGTGGAGAAATGGAGGGGTGAGGAGTCCAGGAGGGCTTATTTGAGGGCCTTTGCCACTTGTCTCATAGCGAGCTCGATCTCCTCATCTCGACAGGTGGAAGCGAATTTCTCCCGGCGGTAGGCA
WI-19946	122	C T	---	---	---	CAATGGACTGAATGAGTGGTGGTGGGTGGGGCGGCACACACACCTTCAATACAGTCAAGGTGCTTCCAGTTTAGAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGGGTCTTCTCCTGACCCAGTCTCTGGAGAGCAAGTCTGCTTTCAAAACCTGCAATTAACCTGGCGCAGAGATTCAACCCAGCCACTCACGAGCCAGTCTGTTTTCAAAACCTGCAATTAACCTGGCGCAGAGATTCAACCGTAGGCATCTTTAATAAAGTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A	---	---	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATATATATAAATATACATCAAGTAACTTACAGCACACATTTTATAGGCCAAAGTTTGGATCTGTCTGGACCTCAATGT(A)CTCTGGAGAGCAAGCCAGTITAGCAGCAGATACCTTACAGCTTGTCTACTCTCAAGGTGATGGCCAAACAGAGCTTCTGAACCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A	---	---	---	TTGGTTGGATCTTGTGGAAAAAAGCAGTTTAA(TG/A)GTATTCAAAATACCTTTTAAAAAGTATTCTAGCACAAAGATTTTCTGTAAACTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAGTGTCGGTTGTAAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTGGCTCCTGAAAACTGCAGAAAGCACTTGTTCTTTAAGATATGGATTCTTTTATCTT
WI-20218	26	T C	---	---	---	CCACACCTCTGTTTTTAAAGCTA(T)CJAGGACAGAGAGATGGAAC(TGAAAAACAGGGTAGAAAAACATATAATTTGGGGAACAGTGGGATGCAGAAAGATGACAACGCCACATGTGCCCAAGTCAATACITTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTACTGGCTGGGATCCTGCCATGGATGCAGGAGAAAA
WI-20295g	154	T G	---	---	---	CAACCTTTTGACAAGGGACGTGAATTTCTGATGAAAGTTATCTTACCAGTTTAAATTCATAATTGGAACTTCTCTTTTAAATATCTCAGGCTTGAATTTGGGAGGGCTGGGCTCTACCCCTTCTCTTCCATCCAGTCTATTGCCAGAT(T)CCAGAGAAAGCGGGAAGCCAGCTCTCCAGCATAGCCACTGTGGGTCCGCTTCACTCTGTCCACTCTCTCATGCTGGACTTGTCTTTCGGGG

WI-20361a	192	GA	---	---	CTGGAGTGTGACCTAAGTGACATTTTTTAAATGCCAAATACAGTAATCTCAAGCTTTTAAATGGCTTATGCAAGATATGAAATCTGATTTGCCAGAGTTACACTGCACTGCCACTCCAAAGCTACAACAGTGCACAGCTGAGAGTTTCCCTATCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTCAAATGGGAAATTCCTAAGTACAGAGACAATGGTGCTACAGTAGGCCCG
WI-20572	75	A	---	---	GAGCCAAACCCAAACAAATAAACAAGAACTCTTTTGTAACTAAGTCAATACCTACTTTCTCTCTCAGAAATTA/GTTCATAAACAATCATCTTTACAACTGGAGCGAGGTAGGCCATAATTTGTTCAAAATTCATCTCTCAAAATTTAAATTTGTTTAAATCCCAAGGTGCTATTGAATTCCTCAAAATAAACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTGATAT
WI-20588	133	GA	---	---	CATGACAAAGACAAAGATCAAGGAGTAACAATAAATAAGTTGAATAAATAGTATACAGCAATCTTACTTTTAAAGAAATGTGAGATCCTTTGTTGTTTTTATTCCTTAAGTACAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCAATTCAGG
WI-20593	79	A	---	---	TGACCTCATCTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGCTTTTTCAGTCTGTTCGTACTTCAGTAAATCTGGAATCTGGGAATGAGCATGCAATGCTCCACCAGATGAGGAGAAAGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCCCTTCAACAGACTATCCAGAAGCCATTCATCGGGTATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57	T	C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGATACCTTGCTCCTCAT/CJATGTATCTGTCCCTGCTCTTTTAGGTAGCAAGGTGATGAATACTTTTAAAGTTTGTGTTCTTTTCTCTGCTGGTATCAGTGAATACTGATCTCTGCTAGGGTCAATTTACAAATTTGCCATGGAACTGAGCAAAAGCCACGTGGGATAAAATCCTCACTCACCATCGAGCCACCAGTAT
WI-19066i	239	A	G	---	TGACAAGGGAGAGAAGGAAATCTACTCTATTCGAAGGAAATCTCCTCACTTAAGCTTCAGTGAGCCCAAGCACTTAAACCCATGAACTCAGCTGATCGTCTTACCCAGTCCCAATCTCTACGAGAACTGGCATATGTTCTTGGTGGTACCCCTGACCTGATGCTGCTTACCTCCATATTCGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTGTTCTTTTA
WI-19066g	184	C	T	---	TGACAAGGGAGAGAAGGAAATCTACTCTTTCGAAGGAAATCTCCTCACTTAAGCTTCAGTGAGCCCAAGCACTTAAACCCATGAACTCAGCTGATCGTCTTACCCAGTCCCAATCTCTACGAGAACTGGCATATGTTCTTGGTGGTACCCCTGACCTGATGCTGCTTACCTCCATATTCGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTGTTCTTTTA
WI-19066f	148	T	C	---	TGACAAGGGAGAGAAGGAAATCTACTCTTTCGAAGGAAATCTCCTCACTTAAGCTTCAGTGAGCCCAAGCACTTAAACCCATGAACTCAGCTGATCGTCTTACCCAGTCCCAATCTCTACGAGAACTGGCATATGTTCTTGGTGGTACCCCTGACCTGATGCTGCTTACCTCCATATTCGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTGTTCTTTTA

[illegible]

WI-19236	54	G A	---	TACACAGGGTGCACCTTGACCTCTGAGGGTTGGGTGTGGAAGGGGAAAGGG(A/G)GATGGAGAC CTGCTCCACAGCTCTCTGCTACGCCGGTTACATGGGAACAGGGTTAACATCTGTGTTAGGGGAGGT CACCTTACCTTTTTCATAGGGGAAGGTGTACACACTCTGTGGCTATCTCAGGGGAATGGGGAAAG AATCTTTCAAGGGCAAGAACTCTGGGAGATGCTGTGTATGTATACT
WI-19144	222	G C	---	GTGCCAGTCTTCCAGAAAGCAAGACTGCCCCATTACAGCCTTGCTGACCTCCAGCCCTTCTAAGG CTCAGCCCCACGGGACTCTGTGTGGCTGCCAGCTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTCAGGAGCTTGCACACAGGGAGCTGTAGCCAGGAACCCCTCTCTTCCCTGCTGT CTGGCTCTGCTGGAGCGG(G/C)TGGGAACCAACACCTTCAGTCTGCTGGTG
WI-19139b	110	C A	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACCTGTATTTACACGAGGGTAGAC CTGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCA/ATATTTACGGGGTGGGGCAC ATGGGTGTGGCACTCTGGAAGGTGTGCAGCAITGGGCGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCGGGAGATCTAGCATCTCTGAATCCTGGCTGTGCGAGGCTTTGAAG
WI-19139a	66	C T	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACCTGTATTTACACGAGGGTAGA/
WI-18910	112	T C	---	CTTGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCA/ATATTTACGGGGTGGGGCAC ATGGGTGTGGCACTCTGCAAGGTGTGCAGCAITGGGCGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCGGGAGATCTAGCATCTCTGAATCCTGGCTGTGCGAGGCTTTGAAG GGCTGGGACCTTTAGGAAGTGAATGCAGGTGAGAAACCTTAACATGAAGGAAGGGTGCCCT CATCCAGCAACCTGTCTGTTGGGTGATGATCACTGTGCTGCTTGTG/GCCTCATGCGACAGCAIT CAGTCCACCGGTTTAGG
WI-19235	173	A G	---	TTCAGGAGGTGGAGTTCCTGCTCAGCTCTCTGCTGTGATGTGGAAAGCTTCTGATATTTGAAGAAACA CGAATGTCTGTAGCTTCCTGCTTCACTGCCCCAGTATGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTGCCTAATGTTCAAAATGGTGGAAAGGCTTCATGTAATATGATCAGGACCCACCC TCAAGTCTCTGAAAGTGTGACAGTGTCCAGCCGGTCTGCGACACTA
WI-19222	179	C T	---	CGTTTCCCTAACTCACCCAGTTTAGTTGGGATGATTGATTTCTGTGTGTGTGATCCCATTTCTAA CTTGGAAATGTGAGCCTATGTTTCTGTAGGTGAGTGTGTGGGTTTTTCCCCACACAGGAAAGT GGCAGCATCCCTCTCTCCCTAAAGGGACCTCTGCGGAAC/GTJTTCACACCTCTTCTCAGGGAC GGGGCAGGTGTGTGTGTGACACTGAGTGTCCAGAGCAGCACTT
WI-19117	134	A G	---	AAATATGTCAACGACGAGGGAGAAAAGAAATGCCTAAGACAAGAACATCTCTCATAGAACAATTG ATCTGTTTTACGGGAACAACCTTGCTTGAATTTACAGAGTGAGACTGTACATAATTTGATGAA A/AGTGTGCTAATTTTCTTAAGACAATTTTCAATTCATGAATATTTCAAGTTTTTCATACCTGTACA CATTTCTTAAACACATGATACGACGCACTGAAATGAATGCGCGAAATTG

WI-19134c	263 C T ...	---	CTCCTGTTGTTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCCTCTATCTCTCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCAGCAAGGGGTGCGCCAGGGGTGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTCTTTTCAGGCAC TTCACTCCACTTGCCTCCTCTACCTCGGCACCTGGGTGGGAAAGGG
WI-19134a	162 T C ...	---	CTCCTGTTGTTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCCTCTATCTCTCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCAGCAAGGGGTGCGCCAGGGGTGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTCTTTTCAGAG CACTTCATCCACTTGCCTCCTCTACCTCGGCACCTGGGTGGGAA
WI-19224	112 C T ...	---	GGTTTCACCACTGCTTCCAGGGAACTCCGATGAAGTGTTCACCAAAATGAGCGAGTGAAOCAAAGA AGAGGATGACATTTAGATCCAGGAGATACAAACAGAGGAGATATCTCTCAGGATGCCCTGTGAAGA AAGATCCCTGGATCCAGGAGATATAGGCAAGTTGTCATATCCAGCAGGCCAGAGACTTCC AGGAAACTCATTTCAAGGAGGTGAAATGATGATGACTGCTCCTCAAGATGAAAA
WI-19201	179 T C ...	---	GCAGCTCTAAGGACCACTGCGCATTTGCTTTTGTGATGGCATCTCTTCCACCTTGTCTTCTC CTTTGCTCCTGTGTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCCGCCCCACACTTTGCTGCAAGTGCACCGAAAGGACTTCTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAAGTCAAGACTCCATGCTGCTGGCTGGCTCA
WI-19034	45 T C ...	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAAT/CJACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAAAGTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAATTTTGTG CTAGCCCATGATCAATCGACTTCTATTGTTTGTATACACTCAGCATTTAAGTTCTGTGCAATTGAC ATTTGCTACTTATAAATTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25 C G ...	---	TGTTCTGAGTCACTGAGGAGAG/CJCTTCACTCAGGAGTTCATGCTGAGATCATGATCATGATGATCA TGCGAGTATATTTTCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAACTCCTGTAGTTTGAACCTCAAGGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGCTTTGCACTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ...	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCCTCAGTGGGGA/J GIAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ...	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCCTCAGTGGGGA/JA AAAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ...	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121 C T ...	---	CAGAGGGAAAGTTTATTGATGAGCCACAGAGGAAACAGAGAAACAGACACAGGAGTTCTGTGT GCATGGGAAATCAGGGGCCGACAGCTGAACCTGCCAGGACAGAGGGGGC/CJTGACAGCA GGCATGCCACAAACATTTCA

WI-18017	87	C A	---			ACAAAGAAATGGAATAGTTTGGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGCAACCCCGGAACA(C/A)ACTGCTGGATAAATCGTTCAATAATATATCTCTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---			TTATTCGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTAGAAACCTCGATTCTGAATATCC(A/G)GTGGCGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGATTTGTGTGACCACTACACAGTCAATTTGTAGAGCATTAATCACT/C JGCCAAATTCCTCTTCTTCTGTAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117	C A	---			CAATGGGTGACTGAGTGAATAAACGCATATTGAGAAAGAGCGCTCTGGCNCCTCTGGTCC AAGGTGTAAAGTCTCAGGATTGCTGTAAGTGAGCCATGAATGCTG(C/A)GTTTCAACCTTTC CTTGGTGGTTCTTCAG
WI-18295	40	C T	---			ACCACATTTTGTGAGAGCCTATTGTGGAGAACAAACAG(C/T)TTGGGAAGTAAAGTTGATTACT TCCTCCAAAGGATGATGTTTAATGAATTCCTTTNCCITAGCTTCAATTAATGCCAAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTTGAATAAAACTCCAGGCTGTGACACGGTGGGAGACACAAAT/ CJGAGTAATTAACACATAATATTTANATGACAGTGAATTAATTAACGCTCGGTAAAGCCAGAG GGGAGAGGGGGCTTTCA
WI-22585	56	A G	---			TTTATTTAAATTTGCATCCTGAGATAATAAATTTATCTGCAAGTGAACAATG(A/G)CAGAAGC AGCAGTGAAGTTTCGGAGAGCAGGTATCTTCAATTTTGGCACAGCTGTATATAGATGA
WI-21155	36	A G	---			GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC(A/G)TCTGTAGATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTGTCTTTTCTGCTCAGAGGCTCAGATGATACGACAGCAACTTCTTTTGAACCTTTTAT TTCTCGCAGGAAGAAGA(G/A)GGATCCAGCAGTGAGATCAGGAGGTCTGTGTTCACAGACAG GGAACAGGC
WI-19888a	98	C T	---			GGCAGATTCACCCATAACAGAGAAATACTCCTATTGGAAACAAGGTTTATTTGTATATGATG AAATATTTTGAACCTAGAAAGTAGCAGTGA(C/T)TGGACAACTGTTGAAGATATTAATGCCACT GAACGTGTTCAATTAATGTTAATTTTCATGTTATGTTATTTTCACTCAATTAAGAAATGGAACATGT CTTAATTTGTAATTTACATGAGANCATATTTATGTTGGAAGTGAACACAAAG
WI-21485	82	C T	---			TGAGACCATCTCTCAACAAGAAATCAGTTCAGCAGCTAATTTTCCACACTGAAAGTCTACG CAATTTTCATGCAAG(C/T)TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAAT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTCCACTGCCCAACCAAGAAATTAATGAATGCNCTTACAATTTGAGATGACTT GAAAGTTAAAGAAAGGTACCTTCTTGGAGGTGCAATGACAGGATTGCTCTCTGTTTCTCTGGT GCAAGTTTGAACAGTATGATACCATTCATCAGAGCATCTGTTTCCCTGTGCAGATCCCACTAG

WI- 20561b	94 T C ...	---	CGTTGCTATTAAAGATGGCTGTTTAAAGTATAAGCAGTTTGAGCAACACTGAITGTGCTATTG TACTTCAGATGAAAAATCCTTACATGT/C/GGAATCAATGTCTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ...	---	CGTTGCTATTAAAGATGGCTGTTTAAAGTATAAGCAGTTTGAGCAACACTGAITGTGCTATTG TTGTAATTCAGATGAAAAATCCTTACATGTGAATCAATGTCTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ...	---	GCCTTCATTTCTGTACCCACCCCTGTCCACAGTTATGTTGGCTTCAATATATGGCGTTAGAAT AT/ATATAATCTATATCATATATTTATACACAAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ...	---	GCCTTCATTTCTGTACCCACCCCTGTCCACAGTTATGTTGGCTTCAATATATGGCGTTAGAAT CATATAAATCTATATCATATATTTATACACAAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ...	---	GCCTTCATTTCTGTACCCACCCCTGTCCACAGTTATGTTGGCTTCAATATATGGCGTTAGAAT CATATAAATCTATATCATATATTTATACACAAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ...	---	AAAGATTTGCAGTCTGGGACACAGTTTGGAAACACTATTTAAGGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGCT G/ATGTGAACTAATGTTTAAAGTTAGAGCTTGTCTCAAGTCAAGTCAAGTCTTAAGATAATAAT ACAGTAACACTACTTTTATTTCTTGTCTTTTATCCCTTTCAGGTTTCGATT
WI-21444	39 A G ...	---	CTGGGACGCAAGTAACCAATTTAAAGAAATCTCTCAAC/AG/AGTCTCTTTTATGGGTAATTC GTTGTTACAAAGTTAAATACCTTATTTGGAACCTAATCTTTGTTATTTATTCGAGGAAGAAATCT ATAAGATTGACTTACTCATGTTGACTGGTCTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ...	---	AGAATGGACAAATGATGAGATGTTGTGAGCATTTTGTAGAGAAAGTGGTATTAGAAGGATACAG CATAAATTAATTTGTAACATGCTTATCTAGCTAACCTAATCTTTGTAGAAATTAAGTGGTATGG GAGATTGGATAGAT/CTGCTAACCTATCTCAATTTTAAATGATGTGAGCAA
WI- 22091c	205 G A ...	---	GGCGTGTATTTGATGCAATGTCCAAACAGTCAAGTATCATTTGAATCCAAATTTCCAGTAGAG ACATGACAGCAATGTCAATGTAACATAACAGCATATACCTCCCTTAAAGTACTCAATTTT ATTACTGTGCTGAGCTTTTAAAGGTTTAAAGTGTGTAGCATTAAGTGGTATTACTTGGGGCA ACA/G/AAATTACGGCTTAACACACACTAAATCATGAGGCTCAGGGAATTG

WI- 21805a	45 A T	CAACTGCTGAGGCTTTTCACTAGCTGATTATAATCCTATATTAA/AAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACITCTCAAGGGTGGATATGTGGGAATGCAGACTCATCATATGTGTGGTT TTGTTTGGCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTTCAATAAATTCGAACAGTTGAAGGCTGTTTGTAAATTGCTG
WI- 21778b	155 T C	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCTGTAACCTTTTATTGAATTATTGAC TCTGCCCCGGTGTGCTGTTGGTCTTCAACTCAGTCTGTCATGTCOCTGTGTAGGTGGGGTCCCCAG GTCTGGGCTTCTGAGGTCTCTGAGGTCTCTGAGGTAGAGGAGGCGAGGTGGT
WI-20907	241 A C	TGAGTCAGTGTGTCAGATGGGCGAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT CAATATCTAGAGCTCATCTCTTGGGCGTACATGAGGGGCGAGTTGTTCTAGTACCCATTTAGCCG ATGGCTCTCAAGCCAAATTCACACTGGGAAACACACCCCTCACAAGATGCCTATCCATTGAGTTG ATACAGGTTTGTAGTCTAGAACTAAAAACATTTTAA/CAATATCTA
WI- 21449b	222 C T	AACAGCAGCAGTCACTTCCAAATGCAAAAAAATTAACAATTTTAGAAATAAAATTATAATGTTTA TAATGGGGTCTAGAGANTTGAAGTACACAGAATCAATCAGCAGCACTGTGGCGGCTGGAG AAGCCAAAGCCCACTGTGTCAGGGTCCAGCTGACAGAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCAC/TTTGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A	GCTTACAAGGAAGCCTGTGTGACAGGCGAGNTGGTGGAAACCGACTCCAGCTGGAAACCTGCCCCC CCATCCCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTCTGCGCCAGGCGAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGAGCTCCCTTCCACAGATGAGGCTAGGGCTGCAA AAGGCCCCGTGAAAGAGAGATGTGTCAAGGCTTTATGSGGTCTCTCCCAOC
WI- 22187b	178 G A	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCTGTTGGGCGCTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCGCTGACCAATGGGTGATTACATTTAAAAACCAACCAAAACAAATAACCAAGA ACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTTCATGAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTTACCCCAAAAGTGTGTGAGGAAAG
WI- 22187a	110 C A	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCTGTTGGGCGCTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCGCTGACCAATGGGTGATTACATTTAAAAACCAAAACAAATAACCAAGA AGAACAGATCAGTTCCTGATGGACATCAGTAATCTATTGGTAATGGTGAATTTTCATGAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTTACCCCAAAAGTGTGTGAGGAAAG
WI- 21609b	146 G A	TCATGAATATGACGCTCCATAATCTCTCTCCCTTGTAAACAACTGTCAGTCCGTTCAAGCTGTAAA AACAAAGCCCAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAGGAGGCTGTAAAG GATGTTTCAAG/G/AJAGGGTCCGGCTATGTGGCCACTGATGTAGGAGTGGAGTGGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTGGAG

WI- 21609a	42	C T	---	---	TCATGAATGTCAGCCTCCATAATCTTCTCCCTTTGTAACAAATC/TGTGAGTCCGTTTCAAGCTGT AAAAACAGCCCAACCCCAAGAGCATCACAGAGGCAAGAGAGTGGCAGTGAAGAGGGAGCCTGT AAGGATGTTTCAAGGAGGGTCCCGGCTATGTGCCACTGGATGTAGGCAGTGAAGTCCAGGC TTTCGTCGTGGGAAGTGGCAGAGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104	T G	---	---	ACATTCGAGCCAGTTTTCATATTGCTCCACTGCCATAAATCCCTGGTGGTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTCCTTTGTGATCTGT/GJACCTCACCATGTCTCCACCTNAGTTCC CACATTTCCCCACGTCCTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139	A G	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTTACATGAAGGGTGTGATGATTGAGCAATCTAGGGGATATGTACAGGGG TTTCA/GTGCAGTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121	A C	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTTACATGAAGGGTGTGATGATTGAGCAATCTAGGGGATATGTACAGAG GGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58	A G	---	---	ACAACATGCTGTTCACAGGGGGAATAATCCTAGGNAATAACTTATGTGTACTTCTTGAGTTC TCATACAAGACAGCACAAAGCACCACCATGCTCTGAGGAACAATTGGACCATGACCCCTTGAAA AA
WI- 18829b	35	T A	---	---	ACAACATGCTGTTCACAGGGGGAATAATCCTAGGTT/AJATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAGCACAAAGCACCACCATGCTCTGAGGAACAATTGGACCATGACCCCTTGAAA AA
WI-20964	87	G A	---	---	AGCCAACTCAAGGCCAAATAATTTCTTAATATAGTTATATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGATA/GJAGACACAGAACTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTAAGATTAGATGAACACACACTCAGAAATCTCTAGGAGAGCTGAAAGAGGAAAC AGATGTTAACAACAATAATTAAGCTGCTGGGAACTGAGTCCATGTTAAGCTTG
WI- 20059a	59	T A	---	---	CTCTGAACATAAGGCCGTGAAGGCATGATTGTTTGGCACACAGAGTGGATACCACT/AJACAT TGGCTGGAATGAGGTGGTCAAGGAAATAAANTGCATACTAACCACTGTGAAATCATGCTGGA GTTCTGGGAAAGTTAAAGTGAATAATACAAAGACTGACATGCAACTCTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165	C T	---	---	TGTTTTTGAGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCTTCCCTCTCTGACAC CAGCAAGGGGAGGCCACCATCAAGCCCTGCCCCATCATGCAATCAATGATTACTAGCAGTAGGAA GCCAAGGGAANAGGAGCCCGCGCTTGGTCT/GJGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGTCCTCATGTCAGTCCCTGTGATGGGAATGAC

WI-21661	117	GC	---			GCCTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAAATAGCJTTTAGTCCACAGTC ACACAAAACCTACCTTTAAGGAAACCTGTCCAGTGAAGCGTTAAATTTGTCTTCAGCTATGAAG GA
WI-21980a	25	TC	---			TCAGTTTAAACACATTCATCAAGGATTCJAGATTAAATTAATGTCAAGTGAGCATAAAAGGGAGATT TAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21638	71	AG	---			TGCTGTGTTAATGTGGTGTTCATTATCTTATTTTCACAGATGGAACAGAAAATACCAGCTTTT AAA/GGTAGCAATATCTATTATTAATAAATATTGAATAACACCATAATAATATCAGCTAAAGGA AGTAATCTAATGTGTTGTTTTCAGAGAGGGAGAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAACTGAAGGTGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	GA	---			TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCAGCTCATTAGA CAAACAGTAAACATCTGGACACGGTTTCAGGCGATGAAGGATACAGJACAGTTAATTAACCTAAAG GAACAGAGTCCCTGCATCTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTGCGGCC AAAACCCACTGAACCTACCCACGCTGAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97	CT	---			GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATAGCCCTGATGTACGACCTTCGCGTCATCTTAT AATGGTTAATAACAGCATTCCTGTCTACCCCTCTGATGATGCTTCTCTCTGCAATGAGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTGCAAAAGATTTCCTGACTTTCTCCAACTTCTCCAACTTCTCCAGGGGATG
WI-21524a	35	AC	---			GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATAGCCCTGATGTACGACCTTCGCGTCATCTACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGAGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTGCAAAAGATTTCCTGACTTTCTCCAACTTCTCCAACTTCTCCAGGGGATG
WI-22652a	32	GT	---			TTACCTTCCAAACCCAGGCCACTTTGGAGAAAGGTGTAAGAGAAATGCTATTATTAATGAAGCAAGAC AATAGGACTACTGGGTAGAACCAAGATGGGAGTCCACCATACACCATCATCTCTGCCACAGAACCC TTTGACATGCTGCCCTCCCTACTCCGCACTACCTGCTAAATGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	AG	---			CAACAGGCTCATGAAACAGAGCCTAGGATCCAGGAGCATAGGAGGTGGTGGTGGGAGGGCTC TGATCCCTTTCTCAGCAGACACCATCTTCAACCTCCCTGGGAAAGCAGCATTTGGAGCCCTACACCA CTTGTCCTTTCTCAGCAGGGTAAAGAAATGCGAGTATTTCAGAGGGGAGGTGCTGGGAAAGJG TGGCAGAGCAGCAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI- 21703c	134 A G ...	---	CAACAGGCTCATGGAACAGAGAGCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGTGGCAGGGCTC TGATCCCTCTTCTCAGCAGCAGCACCATTCTCACCTCTCGGAAAGCAGCATTTGAGCCTTACACQ AGJCTTGTGCTTTCTCACAGGTAAGAAATGCAAGTATTTCCAGAGGGGAGTGAAGTCTGGGAAAG TGGGCAGAGCAGCTAGGGCAAGGACTTAAGGGAACTTGTGGGGGAAGAG
WI- 22883c	139 G A ...	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGCGAGGTGAGCCGGGCTCTGCTAATCTTATC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACTGGTGCATTACAG GGGAGAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAAATCCGTGTGAATGTGGGT
WI- 22863b	55 C T ...	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGCGAGGTGAGCCGGGCTCTGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACTGGTGCATTAC AGCGGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAAATCCGTGTGAATGTGGGT
WI- 22863a	38 C T ...	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGCGAGGTGAGCCGGGCTCTGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTTGCACTGGTGCATTAC AGCGGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAAATCCGTGTGAATGTGGGT
WI-22668	99 A G ...	---	TCCTTTATCTGCTGCTGCTGAGTATTTCTGGGAATCCTACAGGATTTGAGGAGCCCTTGGGATT CCAACTTAACAAATTAAGTTTCTGTAATAATTJAGTTCTAGTCCATTAGATTGTAAATGATCTAA ATGGNGTAACCAATTAATATCAAAAGTATACAGCATTTAAGTCAGCTTTTCGAAAGAACTTTTATT
WI- 22631a	52 T C ...	---	AAGATATAGTGGCAGGACAAGATTGGTCAAGAAATCCTGGCTTCAAGTCTGATTCJAGCACCATT CAAGTTTAGGCAAGGATTTAACCTCTCAGGCTCATTTCTCTTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157 G T ...	---	AATCCACACTTTCACGAGGGGACACAGCTGCCATGTCCTCCAGGCTCACAGCAGCCGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGAGATGGTGAACGCGCATTTGAAACCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTCAAGTTCAGGTTGACGAGGTGCTGCGGAGGCGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTAOC
WI-22714	212 C A ...	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTTACATTTTGTAGAGAAATCTAGGGTCT CTGAAATATCTAGTACTGTTTCCACTCTCTGCTCACTCTGACAGGAGTGTGTGGGAAACGAGT CTGAAAGGATTCAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCACTATGAGTAGGGGCCAAACATCTTAAACAGCTAGTTGCT
WI- 22734a	44 G A ...	---	TGGGGCTACTTTAGATGGATGGCTCAGGGTCTGGGAAGGCTTGATCTTAAAGACATTACCCA AATGATGAGAGGCCAGCAGTCTCGAAGCCATAGTTTGGATGGCAGACATTTTCCGGCAGAGGAAT AGCAAGTGCAGGAGGCTGAGGGAGGAATGAACITGGGCTTCTCTACAGGGTGAAGCGGCGCGGT NTGGCTGAGGTTTGTAGTGATG

WI-22724	117	A G ---				TGATATGATGCTGAGATTGCTCCAAATATGCCTAGGAAGGAAGGTGTTTAGAGATAGGA CAAAACAAGATTGTCAAAATGTATAGTAACCTGTTAAAGCTTGCTAAGGGT[AG/G]TTATTCTATTTT TGGGATATGTTTGGGAAT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAA[AG/G]GCTCATACAAGGT TTGGAAGACCCATCTGACTACTAAGGAGAGTCAGCATCTGACCAATCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTCTTTAGTTCATGACGTTTATCAAAATGTGTGCTACTGTTTCCATTGTTTACATCA/GTGTGA GGAAAGGGAATAAATACTCCCTAAAGGGGAGCAATAATTTCTGCTTTGAAATCCCTTCAATTCAGGCAAA TATTTGTGAGCACCAAGGGCCAGATGGGAAGTGGGATGATGAGTGTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATGAAGTGGCTATGTGACTATGATAGACCAAGAAAGCTACCCAGTCTGAGGAG CCTAGTCTCTCTAAATGAGACAATGTACCCATGACAAGGGCTACAGCTTGCTTTAGCAACCAGGA GGATGAAGAC[CT/G]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCAAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCTCTGCTGCTTGAAGCCCTCATCCCAACCCCTCCAAAGCCCTCATGCCACACACCGTGTCCACATT CCCCATCCTCCCTGCTGCTCCCATCTCAAGTCCCAATTCAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAGAGGAGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGGCTGTGGGTC CT[AG/AT]TGGCGTGGTGATGTGGGGCCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[CT/CT]CTGGTCCCATTTGTCTCCAACGGTGGACAA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGAGCCGAGAAAAACACACACA
WI-21314	122	A T ---				CCATATCAGTCTCTTGAAGCTTCTATGACTTTTAGGTTTCAAGTTTATATATCCTTTTCACTAT GACTTTTCATTTGATTTTATTTGTTTCTTCCATTTCTGTCAAACTTTTC[AG/AT]TTTGTATTAA ACTGTTTCTAAACTTCACTTAATCTCTATCTGTATTTTCTGTAGTTCCTGAACTTCTTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAAATCAGGTTGAGGTTGACTAAACAGACTCTGGACCCACCCAGAGCTTCT GATTCAGTAGGCTGAGTGGGCTTAC[AG/AA]TTAGTATTTTGAAGACCTTCTTAAGTGTTCAG ATGCTGCTTGTCCGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTCTTTTAA GGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATATGATTTGAAT
WI-21187a	94	A G ---				CCACGATACTATAAAGAGAAAAATTAGCTTTGAAAAACAATAACATATTTAGTAACACACATT CATTTTATAAACACACATAAAGACAC[AG/G]GNTCTCAGATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAAGCCCATTTGCATCACTAGGGGAATTCCTAAATGCAGATTCTCAGGCC CTAOCCTACTGACTACTGAATCAGAAACTCTGAGGGTGGAGCCCAAGCAACCTGT

WI-21190	39	T C ...			TTTCCCCACATACCAATGCACCTGTTTGATATAAAGTATTC/GTGGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATATATTAACAATAATTAATAAATCTGTACTATTACTGC TTAGTTATCTAGTGTTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186	G A ...			ACCATGTGCATTATTGGCATAGAAATAGTACCAAGAAATGCAGCANCTAACTTGGAGGAAA GAACTATTGCACAAACCAACATTGTACATATCTGATTTAGACAAGCAAGCACTTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGATGGTGTGTTCTCCTCAGCAAGTCTGATCCAACTTC CAAAAAGAGCAGTCATTGAAAATGCTGACTTATGCATTGCCCTCAGGAAGAA
WI-19937c	185	C T ...			ACCATGTGCATTATTGGCATAGAAATAGTACCAAGAAATGCAGCANCTAACTTGGAGGAAA GAACTATTGCACAAACCAACATTGTACATATCTGATTTAGACAAGCAAGCACTTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGATGGTGTGTTCTCCTCAGCAAGTCTGTTGCCAAACCTTC CAAAAAGAGCAGTCATTGAAAATGCTGACTTATGCATTGCCCTCAGGAAGAA
WI-21117b	227	C T ...			GAAACGGGGTGTAAACAAGAAAGTCTCAGATCCCACTGAAATCTGTTTCAGTTTCACAGGCTC TCTCAGAAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTCTGGGG TCCAATCACATACTCAGGTTACAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTTATTTCTTCTACTGAAATCTTGGGTGGAG
WI-21122a	42	C T ...			TCACTTTGTATCAATAATCCCTGTAAAGCTAAAGTTATTCAC/TTTAAAGAACTCTGTTTTTC TTATCAATGTACAAAGCCTGACGGCTTACTGTACATATTCAGTACAGGAGACAACCTGGAATACT AAACAATACTGGAATTCACATTCAGACAGACGAAACCAACATGGATGCCACACATAACTTCCT TTGTAGGTTTTCACAGAGAGCCTATTGTTGGGTTGCT
WI-21254	53	A G ...			CAGTTTGTACAGGAAGGCCCCATGAATGTGGCGGGAACCTATTCACAGGAGAG/AGCAAGGAGAAG CTGTCTCTGG
WI-21054	23	G T ...			AAGGAACTGCATGGGTACAAATGTTTCCAATTCATATTAACAAGGTGGGGAACGGGTCTATCT TGGCTGCTCAGAACACAGGGGGGAGTCTATGCACTCTG
WI-21059b	181	T C ...			GGGACAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGCTTGCATTTCCAGCTTCGTACACATCTTAATTTCAAGCTGAAA AATCTGGGGGAAGACATCTTCACTGAAGTCATTTCTATTTCT/CAATTTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCTTGCCTAAT
WI-21059a	63	C T ...			GGGACAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGTT GAACTACAGCTGCCAGCATTTCTGGCTTGCATTTCCAGCTTCGTACACATCTTAATTTCAAGCTG AAAAATCTGGGGAAGACATCTTCACTGAAGTCATTTCTATTTCTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCTTGCCTAAT

WI-20442	37	T C	---			TCCACGTGAAGGAAGAAAAAANGGGGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAGTGCAGTGAAGACGAA CA
WI-21235	43	T C	---			GTGACAAGAGGTGAAGCAAGGACAAAGGGGACAGGGGAGTGT/CJCTGGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C	---			ATCAGAACTGCAATCTGCACATGAAGAAGCTGGGGGAATGCTACATCTGGAAATTT/CJCATTAAC ATCAACGTAAATTTGTCCGACCAAGTCTTCATTCGTGATCAGTCTTTTGATATAAGACAGATCCAAACAT GAAACTCCTGAAGCAAAATGAATATTACCTTGTGCTTTTCATGCAAAATTTAGGACCAAACTCAAAGG TTTCATCATGCTGGGACACCAAGATCTAAGGAATGTGACAGGGATCTTCT
WI-21149a	167	G A	---			AGGACCTGCTCTACACGTTCCCTACCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCACCT AAATAGTGGCTTTTCTTTTAAACAATGACCTTATTTTATCTTTTAACTTTAACTGAGTCTTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACACGATGCTTCAGATGCGGCAGTATTCACAAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAAACCCAGGCTCTACCTG
WI-21376b	188	A G	---			GGTGCAACTTGGAAATATGGTTTAAACAGGATAAGCATTAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJBAAGTATCT GAACTGAGCACGCACTCATGTCTGCATGGGAACCTCTGGGGAGAGAGCCT
WI-21382d	125	C G	---			CCATTGCAGTCCAGAGATGAGAACTGGACCAAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAGTGGGGCGGGTTTGGATCCAGTGGGATNGGCTTCCQ/CJAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCAGCAGTCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAAGGTCAGGTCAGGAGAGAGCTGCTCCTCATAGTCTCGCAC
WI-21437a	201	G A	---			TCCCTGAGGTTGGAGTCTAGCATAGTCCCTCCCTCAAGAGGGACAAGGGGTCAAGGGGACAGC AAAAATCCAGTCTGCTTCAACACGGAGACTGCCCTTTGGATGGAAGTTTCTGAGCTCCCTCCATT CTATTCTGTGGGGCAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGTCACTTTACCAGGGQG /ACAGGCAATGTTGGGCTGCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156	A C	---			CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTCTGTATAAGCTAAATATGT/CJGA GTTTTATGAACATGTTTATATAAAATGGTCAACATATAATTTTAACTGATTTTAACTGATTTTGA AGGAGGAGAGAGTGAACCA/A/CJGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C	---			CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTCTGTATAAGCTAAATATGT/CJGA TCTGTTTTATGAACATGTTTATATAAAATGGTCAACATATAATTTTAACTGATTTTAACTGATTTTGA GGGAGGAGAGAGAGTGAACCAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI- 21627b	153 A G ---	---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCACTTGAGTACCTCATTTAGTATGATATTTATGCTAGGAATGACAA CAGTAAAGGGCATTGCAAAAGTGCCAAAGTCATCTAATATTAAACCATATTTACATAAATTTGTAGG GACAGTATACTAATACCTACATAAATAAGGGTTTAAAAATGTGTGCTTA
WI- 21627a	108 A G ---	---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCACTTGAGTACCTCATTTAGTATGATATTTATGCTAGGAATGA CAACAGTAAGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTACATAAATTTGTAGG GACAGTATACTAATACCTACATAAATAAGGGTTTAAAAATGTGTGCTTA
WI- 21399a	75 C T ---	---	---	GGATTGAGTCCCACTTGATCTCAAAATCAGCTTTTCATGTAACAAAGCTCATTCCTCTAAAGTT TCAGTTTCCTTACCAGTAAGGAAAGGTTGGACCAAGACATGTTGGACCGTAATTCCTTGGTAA CTGCCTTCGCAATTTGCTCTGAGGTTGTGTCTCCTAGGACTAGGTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGGCCAATTCATCTGT
WI- 2032c'a	68 G A ---	---	---	CGATGCTGCTGATAGGAGGTTAATCTTACATGGTGGGTCACAGAGACAAAGACATCAAT CIGATCTGTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCATCTATGAGAC AGCAGTGTGCTGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCAATCAATGTACATGTAATCCAAATTTAACAGATCAAAATTTACACTAAGTTTCAGT TAGTATCTAAGTATCCAAATCAGCAATTTGATCTAAGTTTCACATTTTAAAGAAATTTAAAGGTAAT AAACTCTAGGTATACCTATTCATGGAATAGTTTATTCNNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGCCAATTTTCAGCTGTTTAAAGGAATTTAAACATTTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATACAGTGGGGGCAAGGCCGCTCCGCTCCAGCTGGGTTTCCC AGATGCAACAATCTGCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCTTCGAGCTCT CAGCG
WI-21242	115 G A ---	---	---	CTGCACCCAGGGAGGACAGCTGTCGAGGAGCTAATAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGCGGCGAGGAGGAGAGCAAGCACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI- 21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGCGAATNTGAGGCTGGGTGAGCTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTACTGCTTACTTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGAGCTGGCTCTTTTGAGAGAGGCAJAGJAAAGGCAAGCAGCAAC ACTTAGGAGCAAGACCTTCCCGTCTCTCCACCTATTTCTCCCTGAGG

WI- 21475b	117 A T ---	---	---	TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGGCTCCAAACCCAGGCTTCATCTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGGAGTGGCTTTGGAGAGGGCAAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTTCGCGTTCTCCACCCATTTCTCCCTGAAAG
WI- 20893d	207 A G ---	---	---	TGTTTGTTCCAGCCACATCTCTCCAAAGGAACCCACCCAGCCGCTGTGCAGGCTTCTGCAGGG CTGCTCTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTCATCAGCGCACTCC AGCGTCAGGCGCAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCN/GJACATAACATTTGGTAGAGTAACACAAACCCACAGCCCTAAATG
WI- 20893c	179 T C ---	---	---	TGTTTGTTCCAGCCACATCTCTCCAAAGGAACCCACCCAGCCGCTGTGCAGGCTTCTGCAGGG CTGCTCTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTCATCAGCGCACTCC AGCGTCAGGCGCAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAACACAAACCCACAGCCCTAAATG
WI- 19941c	71 C G ---	---	---	GAGCTCAAGGGAGACCTTTACCCAGATAGGACTAAGTGGAGGGTGGAGGAAACCAAGGTGAAA GGTATCTGCGCTCTGGTGAGACAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTGGAG GGACACAGCAGGGTGCAGGAGGGAGATGGGGGACATTTCTTATCCAGTGCATGCCCTTAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI- 21552b	166 C A ---	---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTTGTACAGATACACAAATGTG TAATAATTACTCAGAGTAATGCGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATCTCTGATTTTAAATTTAAATGTAC/AAATTAATTTATTTAGTTAGTTACCCC ATTGTGCTATCAAAATTCATCTTATCTTTGTAACATTTATTTGTA
WI- 21552a	66 G A ---	---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTTGTACAGATACACAAATGTG /AJTAATAATTACTCAGAGTAATGCGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACTCTTGTATTTTAAATGTACAAATTAATTTATTTAGTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATCTTTGTAACATTTATTTGTA
WI-21512	54 C G ---	---	---	TCCTGCTACTTATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTC/GJTAGAGAGGA AAGAGCTGGTGGCTCTCTGAGGCAAGCTCAGGTCCGGGAAAGCAGCTGGTCTGTGATCTGTC TCAGTGTGGGAGTCTCCACTGCCGCCACAGGAGCCTCGGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTGGCTGGTGGGCTCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A ---	---	---	CACATAGTTTCTCAAGAAGAGGATGAACGAAACCTCTTAAGGAGGCAAGCAACTTCCATT ATCTTAGTTTAGACCAAGATCTTTAATTTTATTTCTCTTTAATTAACGTGCAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCGAGTGAAG/AGJAGTAG TATCTCTACATACCACAGTATACAATGATGCTTCTCTGAGGTTTAGGAAC

WI-21514b	133	CT	---	---	TTGAACCTCTGAAGGTGGCTTATGCTCGACTCCTCTTCTAGGACTGTGCTATGAGCTGACAAGCATAG AGGCAAGATATCTCAACATTACAAACCCCACTTCACTTCAAGAAAGGAGCACAATTACCATGGAGGCT /TACAGGCTCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGCAAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAATTTGTCAAGGGTCAATAGGAAT
WI-21514a	100	A	G	---	TTGAACCTCTGAAGGTGGCTTATGCTCGACTCCTCTTCTAGGACTGTGCTATGAGCTGACAAGCATAG AGGCAAGATATCTCAACATTACAAACCCCAAGGCTTCAAGAAAGGAGGAGCACAATTACCATGGG GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGCAAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAATTTGTCAAGGGTCAATAGGAAT
WI-22020	27	CG	---	---	ATGAACATGTTGCAGTCCGGATGATTCGTTATCATGATGCTAAGTGAATGAAGCAAGCAGACACAAA AATCCAAATGATCATCTGCTACCTGTATGAGGGTACTT
WI-19576a	113	A	G	---	TTATCCGGTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCAACCTGGCAATGATTTATTACA GATCCAAATAGACTCAGCTTCAGACATTAACAAATTTAACATTGATGCTAGTTGAGTATGAT CACAANITTAACATCTGCCAGATGACAAATTTGGTAAAAAATACAGCTCTCTCCACCGGGA G
WI-21695a	141	A	C	---	ATACACAGCCACAATTTGAGGATGAAAGGCAGTGGGCACTTGGAGTGAAGTACTACACATGGCAATA AGCAGCTATCTCTTACCACCAAGGTTCTTGGGCACTGTGATGGTGGCCAGCAGCCCTTCCAA GGGAATAGCTACTACACTAAGCCCTACACTGTACTGTGAGAGTCACTGGTGAACAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTCCAGANTTCTAAGGCCCAAGCAT
WI-21574a	235	CT	---	---	AAACCCAGAAATTTAGTACTTTTGTATTATGAGGAATCACTACTAGGAAGCAACTTATGAGTG TGTAAATTTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGTCTCAGTGAACAGGCG TCATCACTAAAGTGAGGCTGTCTATCTCATTTGTGAATGTCCTCAGAGTCACTAGGAGGAGCCATT GGCAGGCCAGGGAATCTAGCCCTACTTCTCTGTGCTGTCAGGTGGGA
WI-21644c	151	T	A	---	TGACTGCCAAGATTTAGCCCCCACTTAGGCAAGGCTCACTCTAACCCTTCAGGAAGTCTTGGT GTGACCCACTGCATAATGGATTTCAACATANTATTAAACAGCTCAAGGTGATACATAAGGCTTG TTTCATAAATAAGGAT/ATTCATCAAGATCCATGGATGTCAGTTTAAACATGTGTCTCAGC TTGCCCTAGTACCACCTTCTTCTTAAATATGCAACAGCAGCAAGTCTC
WI-21614b	55	GA	---	---	TGCTTTAACTCAAAGTCCAAATAACATATAGACATTTTGCAAGTATCACAAGTACTTTCAAGCTTATAGA AACCTGATTATGATCACTGTGCAATTCAGTCACTAAATAGCAGCAACCTGACTATTAAATAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCACTGATTTTCTTAAGGACTAGGAGGT GGAACGCTACTACGGGTCAGTGTATTTTGGGAGTGTGGCTGTGTGGG
WI-21615b	151	CT	---	---	GACCGAGAAAACCTGCAAGGCATATGATTTGTGCAAGTATCACAAGTACTTTCAAGCTTATAGA GAACTTGCAAAAGTACAAGATGGCTATTTTAAATTTACATATTAAGATAGGATGGACT CTTTCAGTGAATTTATCTAGGACACAAATCGACGGATGTAATCTATTGANTTATACATAGGCC TATCTATATTGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

WI-22082b	67	C T	---			CAGGACTTGGTTGCTGTCCCAACTGCACATAAATGTCCTTTTGTGGAGTATGGTTGTGTCG /TGTTCCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTGCTTATCCGGATGACGG AGGTACACGGGGCGTCCGCTCAGTTCCGCCGAAGGACGTATCCGCTGAAGTGGAGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	A G	---			AACACAACTCCATGCTTTCAAGATTCCACACCCACAGATAAGACATAATTAATTTACAGCAAT TAAACAGTGTAGTTGGTACATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTCTT/AGTAAAGTGTAGTATACATTAAAGACAGTATTGAGAAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGGCCCTATTTCAGGCTTCTCAGCTCATCCACACATCACC
WI-21723b	125	A G	---			AAGCGATTTTAAATGATTGGACATACCTGTAGGTCAATAATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTCAAAAGGTTAGTCATATCCCA/AGJCAACA GCATGATAAATAATCAACTATGTAGAAATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-21723a	82	G A	---			AAGCGATTTTAAATGATTGGACATACCTGTAGGTCAATAATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTCAAAAGGTTAGTCATATCCCA/AGJCAACA GCATGATAAATAATCAACTATGTAGAAATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-22132	99	T G	---			CAACAGATGCTTGAGCCAAAAGCAACATAGCGAGAATAACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTACTATCTTTG/CCCCATTTCTTAATCTCTTTGCCTTACAA TATATACCTTCTAGGTATCACTCATCTATAGGAATGCCCTCTAGTTAATGTCCTGCCCAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGACAGTGGG
WI-21006a	106	A G	---			TGACAGATCACACCACATTTGTTGTAACCTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCCTTAAAGAACACATACACACATGTCACACAC/AGJAGAGGCAAGTACAAAATGTAAACC CCACAAAAGTGCATGTGAATGAAAGTGCAAAAGGCTTCATTTGCAAACTCTGAGGATCATCTCT CTGCTCAGGAAATAACAGAAAGGTCCTAACTGCCCTAGGCT
WI-21761b	138	C G	---			CTGAGGCTGCTCTAATCTCATNTGACGAGCGAGTTCTCGGCTTGGAAATAACTGAAAGATTCAT TTTCTCTTTGTGTACAAAGGATTCAAATAATTTACATCTCTCTGCCAGTTAAACGTGCCGTGG CTGJCAATACACAAAGCCAAAGCGTAACCTTGGCTGCCCTCAGGAAGGCTGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G A	---			AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGATGCAACTGTGGGCAAAATCAAGTTGT TTTAATACCAGTGTGACAGCTTTGATTCTCTCCATGAAATTAAGCTGTGTGCTCACTTGTACATAA CTCAGGCCACCTGAAATATCTGCTAGTGGG/AGJAAATTTACAAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

WI- 21079a	50 G A	AATGAAATGCCACCAGAGGTTAACAGCTTGCATGCATGCAACTGTGTG/AJGCAAAATCAAGT TGTTTAAATACCAGTGTGAGCTTTGATTCTCCATGAATTAAGCTGTGTGTCTCACTTGTTTACA TAACTAGGCCACCTGAAATATCTGCTAGTGGGAAATTAACACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACATCTGCCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45 T G	TCTGTAGATTTAGCCATGCCATATATTAACTTTTAAAGGAAAGT/GJTTATTAACAGTCATTGCT TGGTAGAATCCAGTCTGTCTAATAGTTAGCTTAACAGTTAAGTGAAGTCTTACCTTATATTTA AATGTTAGCAATCTCTACTACATTTCAAAATATAAATAATTTGGTTGCAAAATTCAGNAAAGGCA TTAACCAACATGGGAGTCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G	TGGAGTTAAGTGGGGCTCTGCTATTTCCOCAAAGAGACTCGGAAGATGTTGATTCAGGGCAGAT GAGGGCAGAC/AJGGGATGAGGCTCTTCTGTAAAGTCCACAGAGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGAGCTCCACAGAGAGCTCTACTGTCAATGACCCACACCCACCTCAACC CAGCACACAGGCACAGCAGGGGACACGACACAGCTGCACCTCACACG
WI- 18916b	42 C T	AATGGCATCCCTGTGATACCAACATCTTCAGCAGCTCAGGCT/GGGCTTCCACTTCTTGTACCC GGTTAACTGCCAGNGGGTGACAGTGTGCCAGGGCTGCGCCACTACTGCACTGGACACAGCCTCAAC AATGCCACCTTCATA
WI- 18916a	35 G C	AATGGCATCCCTGTGATACCAACATCTTCAGCAGCTCAGGCTTCCACTTCTTGTACCC GGTTAACTGCCAGNGGGTGACAGTGTGCCAGGGCTGCGCCACTACTGCACTGGACACAGCCTCAAC AATGCCACCTTCATA
WI- 19828c	200 A G	TTCCCTTCCOCAAAGAGTGGGCAAGAAAGCTTTGTTAACTCCCTTTACAGATGAAGAAACAA GATCAGAGTGTCTAAGTGTGTAGCTAGTCCAGGCTTGTGGGCCAAATCTGGGTCTTCCCAAG CCCATGCTTCTTCCACTTTCTACAATCTTACTTCTTCTGACCTCACCACCACCAAAATJAG JCTTTTAACTCTGGAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI- 21883b	47 C T	CACAAAGTGTGTACAACCTTAGGGACACAGCCTGGGCTGCGCT/JAGCTGCATGCCACCTC ATATCCACCCCATCCOAGCTCTGCGCCGACACCCAGGCTCCCTGCTGTGTGAAGTATTTT CTCCAAGGAGGAATGATCTCTGATCCAAACACAGCATCT
WI-19860	51 C G	TTGACCTAAGCCTAGCATAAATTAGCTAAGTAGAATGTTTCCAAAGATG/JGJGTGCATCAGTAT CTCCATCCACATAATTTCTGTTGATTTGGCATTCACCATTAATATGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGNGCTCTGATCTCTAGSATCTGAAGCC
WI- 19889b	80 C T	ACCCAGCTCTCTACCTCTGGCTTTCAGTAGGCTTGGCTTAATGGCCANTGAAACTGCAGGCAAG AGGAGTGAGGGGCTJTAGACGATTTATTTCCCTCTTTCACCTCCCTGTAGCTTGTGTAGTGCTGTAT TTCTCTACTGATAGTTCTTGCCACAGTGTAACTATTG

WI-19891c	172 C G ---				TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGCCCTCCCTCCCG ACTCTCTGTCTGGGAAAGCTGGCTTGNCTCCAGACACAGTGTAGATGCCAGCTCTCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTCAGCTGCTGCTCCGGGGCTGGGGCTGCTTGT CAGGCAGCGCGGGGAGGAAGGAAGGAGATCCAGGGTCTGCTG
WI-20155a	81 C T ---				GCACCTGTAGGGGTGTAGCTTCCATGGTTCCAAAGCAAGGGCTGTACATACCTTAGGCTGACCAT TCCTTTGGGGGGCTGCAAAAGCTGTTTGGGAAATNTCCAGAGGAAATAAAGTAGAAGACGC ACCTGCTATTTCCACACTACTATGAGAAATACAGCTAATGAGTGTGGGCAAGAGCTTGGCCGTGTGA GTGCCCGAGGGTAAAGTCTCTCTCTGTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---				AGCCATACAAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCAGGATAAGGAGCAT/GJACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAATATAAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTTTCCCGCAGAGGGCTGSGAGCGCAGGGGGTGTGGGAA
WI-20270a	53 G A ---				AGCCATACAAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT AATACATTCATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTTTCCCGCAGAGGGCTGSGAGCGCAGGGGGTGTGGGAA
WI-20622	130 T C ---				CCACTTTCATATTTACAAATGCTCAGCAGCAAAATATGAAAGCTTCAACACTTTCCCTTTGTA ACTTGTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/GJ TACTAATTTTATGATGTTACTCATATTTTATTCATATACCTTTTAAATGACATCATTTGCCAATACATA CATTAATTTCTNTAATTTATTTTACAAATAGCCAAACATCTGTATGCAG
WI-20768b	190 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCTCGGAAGCAGGCTAACAGGACCTCTGCGCTGCGTGC TCAGGACTGATTAATTCATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATCACCACCTTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAAAGTACGACACATACCTGCTGGGAGCTGAGGACTC GTAATGCGCTTGTCCCACTCTCTCTATGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCTCGGAAGCAGGCTAACAGGACCTCTGCGCTGCGTGC TCAGGACTGATTAATTCATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATCACCACCTTA CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAAAGTACGACACATACCTGCTGGGAGGAGGACTC GTAATGCGCTTGTCCCACTCTCTCTATGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---				TGTTGGCTTTGTCAGGACTACTGCTGTACATAAATATCTCATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCAGCTAAATAAAGATATTTGTTGCTATCTTAAAGAAA TGCTTTAACAATACCAAGATGATGGAATCAATAGATAAATAATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAAATAGGATACCACTAAATTTATTTCTTATGTATGAAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTGCTTTCTGGAACATAATGGAACACTTGTTTTCATAGCTGTCTGACAGT GGACAATCCCACCATCTTCAGGCCCTTTTAAAGGTCAATATGAATCTGAATTTCTJAGJTTAAT ACTCTGGTGCAATTCATTTTCATCTGCAAAAGCAACTGGCACACCACTCTTCCGGTGGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTTCACAGCTCAC
WI-22189	70 C T ---	---	---	CCAGGATGAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AATCTGAGCGGAGGAATGGCATGCGCTGCGGTACAGCCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGATCATAGAAAAAAACCCCTCAGCCAGAAGTTAGGCATTTGTGATCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGCTCTGCTGTGTTGTCATTTCGCAAAATAAACCCCA GACCGGGTCATCTTTCAGTTCCCTCCAGCTCTATTTATGATTTGCTCTAGTCTTTATGAGCCA TGATGATTTATCAGTCTCCCTGATGCACCTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGCCCTCTAAGCAACCG GCCAGTGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGGACCTTGTCTTT TCCTTCCAACTCTCTCTTACCCAGCAACTTTGCGAGAGGCCCTTTTNAATTTCTCTTCCCTCTATTC CCTCTTTCCCAAAATGCTAGGTGTCCTAAGTCCCAATCCAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGGAAAGGTTTACAGCCATAGTGAGTTCCCTCCCTGCTCAGTACCAGAGJAGJTTTGATAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGTCGTCATCTCTGCTGGCAGCATCTATACCCACTCTGGCTCTGAAG GCTTGTCAACCAAAATGGGAGCTGGGCTAAGGCATATTAAACAAGGCTCCAAAGGACCCCTT TCCTTGGTCTAGCATCCAGCCTCTCTCTCAGCAAGGCAAGATTGTGTTCTJCCCTTGTGTTTCTG AACAGGCCCGGAGGCGAGGCAAGGCATGCCATCCTGCAAGCACTCAACCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTT GTAGGATGGATGAATGAAGTGAATTAAGTCAAGATAAAGGGGCAACTCTTTAATJAGJAG GAAATGTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTTCCAGCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAGTCTGJACJGATCAGGTGCTCTCCACCAAAAGCAAAACAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTGCTTTATGTTTACAGCAATCAAGNCTGCCCTCCAGGCAAGCCAGTGTCT JCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCTTGAAGCATGGCTGTGTGACCAT ATTTCCCTTCTGTGTTCTGTTATTCCTTTTGTGAGTAAATNAGCAATACAGTGTCTGGA ATCTGCATGATTAAATAACATTAAAGTTTCAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATGACATCTCTCTCTAGTT
WI-21342d	59 T C ---	---	---	T

UTR- 04932-2a	149 C T	GCAGCATTCTCTCCAAACCTCCAGGCGAATCTGGGGCAGAGCACTCATGCGCAGCAGCAC CTACGTGGCCGAGTACGAGCCCGCTGGCCCAAGTTCTGGCTCTCAGGACGTCCACAGATGGA GCCAGAGGTTTTC/TCTGGGACTCCAGCCAGGGGATGAGCCGCCGCCGCCAGAACTGGAGTCTTC TTTGAGGGGGCGGGTCTCAGCTCTCTCTGGGAGGTGAGGAGGAGGT
siFIBb	412 G C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siFIBa	341 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siGLV2	61 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1001	70 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1002	33 G A	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1003	63 A T	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1009	36 G C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1011	107 C A	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1012	89 T C	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT
siSG1017	42 C T	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGGCGCTGACAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACAGGCGCTTGCACCTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTGTGTAGTACATCTCCAAAGATGCGAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTCTAGAACCTCCATGGTT

EST22917	74 C T	GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/TTTGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458	65 A G	CAAGTTAGAACCATGCAATCAGCTTTTCATCCATGGTGAACCTCAGGCTGCCTACTCA/
EST36745	56 A G	GTTGGTGTCTAGCCTGACTGACACAGGAGCTTGAATTTGGAGGCTCCAGTCACTCTCCA GAGGGGAACCTTCAAAGAGATTCCACAGTGAAGCAGATCATGGGGCAAAAGTCA/GTATGG GGCCAGACTGAGGTGGACACACAAAGCACTCCAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGCCAT
STS- R37410c	201 A T	TGTGACCATACCAACCTATGCAATAAAGAGAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGG ATTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATCTGGTATG T/A/JTATGTGAGTGGTGTCTAGTGGCCAAAT
STS- R37410b	139 G T	TGTGACCATACCAACCTATGCAATAAAGAGAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGG ATTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAACATCTGGT ATGTATTTGTGAGTGGTGTCTAGTGGCCAAAT
STS- R37410a	48 C T	TATCGTGGGAGTTCCAACTCCTATGCAATAAAGAGAAAGAAAAATCCTCAC/TTTAAAAAACAACAA GGCTGCTTTTAAATTTGTGCTGTAACTGGGAGAAACCTCTCTACTCTCCACAAACCTGAA CAATCGAAGAGATGCATAGCGGATTTGGTGGCTTTTACAGAGCTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCTCCGGGATGGTGAATAATGTTCCGGACCTAGATA/C/GTGAACGA AGGTAGCAGCAGTGTGAGTGCCTAA
UTR- 04350	125 C G	GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAAATTTCTCTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCAAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAATGTAT
siSG1028	55 T C	GTATAATTCAGCATAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAATCTTTACA AGAT/GJAAAGCAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTTAAAGTTGACTATC
siSG1028	70 T G	CACITTAGATATGAGGAAATGGTTTAAATGGACACAAAGAGTCAAGCCACGTTTGAACCAACATAG TTTCATACACAGTTGAACCATGTGTTTGTATGCAAAATACAGCAAAATAATTTTTCAC/TCA/TTG TCAATGCCAATGCATTGAAGGGCCAGAAATGAGAAAGGATACAAACATTTTGTATAAAAGGTA AGAAATTTCTGTGTG
siSG1031	128 C/A	AGAAATTTCTGTGTG

siSG1033 1b	116 T C ---	---	TTTAAAGCTACATGCTGAAAGATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAACTGCTCTAGGAAGGCTAGACCTCAAAACACCAACCTCCATTCGTCATTCTCTCTTTGG CTACTATGCTTTTCCCTGACTCTGCTCTCCAGCTCTCTGGGCTGCTTCCACCTGTTCACTGTA CTTAGGACCTCC
siSG1033 1a	107 A T ---	---	TTTAAAGCTACATGCTGAAAGATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAACTGCTCTAGGAAGGCTAGACCTCAAAACACCAACCTCCATTCGTCATTCTCTTTGG CTACTATGCTTTTCCCTGACTCTGCTCTCCAGCTCTCTGGGCTGCTTCCACCTGTTCACTGTA CTTAGGACCTCC
siSG1243 b	225 GA ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAATGGTTTTATAATCTCTCTCTTG AAATTATGTTCCAGCCCGCCAGCATGGTAGCTTATGCTGCAATCCAGCACCTGCGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACACAGCTGCGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTCTG/A/AAAGTATTTCAAGCCAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTCTGTCAATAATTTGAAGTATGCTTCTTAC/G/APCGCT TCACATTTTACATGGGCCAAATTCAGGAGATGCCATGCAATGTCATAAATGTCATAAATGGGCAA AACTGACGTATCACAGGGGCAAGTATCTCTGTCAATAATTTGAAGTATGCTTCTTAC/G/CTACGCGCT TCACATTTTACGATGGGCCAAATTCAGGAGATGCCATGCAATGTCATAAATGGGCAA TTAATGTCATCCAGGGGGGCCAGGATGGAGGGGGGTTGAGGAGCGAGAGGCGAGTATTTT TGGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTG/CTCAATCAATGAAGAA GACAAAGGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAACATGGGCC CCAGAGCTTACGCTCTCTCTGCTG TCGTCCTCTTCCAGTCTCTGCGCAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TTCGCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATTGTGTAATGTTGTGTCGTCGCTG GATCTGTTTCCAGACAAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTCCAGTTGGCTTCTGCTCTCA/TGJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGTTGTCACAGTTTCACTGCTCTGAGCTTGAAATCCAGCAGCAAGAGATGCTCACTCCCA AAGTCCATAACTCACTCTGGGAAG CCCTGGAGTTCTGAACATAGGAAGAAATGCAAGTCATGTTAGGTGTCGAGTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCTTACC GCA
siSG1471	50 A G ---	---	CAAAACCAAAATCTTCCACGATATATTAATTTAGTCTAAGTCTTTTAAATCAAGGTTGAGA ATGACGAATTCAGAAATTTCTTACATATAAATGCTTTCTTCTAGTCTGCGATGGGTA
siSG1483	44 T C ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTGTGAGGACAAAGGCAAAACCAAGTGTGCA TCGJAATGTGGAGGATGCTGTTGCAGCTGTAGTTACTAATGCGGGAACCCCAATGCAAGAGGAA AATGCTGTA
siSG1896	67 T C G ---	---	

siSG1847 b	95 GA ...	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACG/GA/TTTACTTACATCAGTTGCGTTTATAGACATTTGAA TCATATCTGAATGACTGACTGTGTTCCAAATGTGAAACCAAAATTAATAATTAACCTGATCAGTGTGCT TCAACACAACTG
siSG1847 a	49 CA ...	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCTC/AICTAAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACGCTTTTACTTACATCAGTTGCGTTTATAGACATTTGA ATCATATCTGAATGACTGACTGTGTTCCAAATGTGAAACCAAAATTAATAATTAACCTGATCAGTGTGCT TCAACACAACTG
siSG1897 a	83 AG ...	---	CTTAATGCCCTCTCTCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCGATGGGAAGTGG AGGAGACACAGGACTG/GGCCACACCTCTCTCCCGTCTCCCAAGATGACT TGTCTTGAGGTTCAAACTGAGATATCTATGGCAAGTTTATAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT/C/ATTCATAATCTCATCTATTAAACATTAACACAGGCCCTTTGTTGT TGTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
siSG2022 a	86 TC ...	---	AAACGTTGTCCCAAAATTTGTTGAGTTTCACAAGTATAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTTATAAACACTTAAGAAATATATTTGACATTC/GJACATCACAGTGGGGCAATTT
siSG2076	104 CG ...	---	TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAATGATTTGAGGGGCTCCACAGAGA GAGC/JG/TAAAGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGTATG GTTACAGTTACACAGTTGTTCTATTGTTGCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTGTTGGGCTGTGCTGA
siSG2108 c	71 AG ...	---	TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAATGATTTGJAGGGGCTCCACAG AGAGACATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGTATG GTTACAGTTACACAGTTGTTCTATTGTTGCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTGTTGGGCTGTGCTGA
siSG2108 a	49 TC ...	---	TTATCCAGGGGACAAAGCTGCACAAAAGGAATGTTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCTGCGATGGCGATGGTGCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGTTGTTGAAGAGAGAGAAAG/JAGJAAGTTCCCTATTATATTAAAGGC AGTTTTCAGAGCACTGGCATCTCTGTTGCTCTG
siSG2141 b	173 AG ...	---	TTATCCAGGGGACAAAGCTGCACAAAAGGAATGTTCTTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCTGCGATGGTGCAGGTGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGTTGTTGAAGAGAGAGAAAGTTCCTATTATTATTAAAGGC AGTTTTCAGAGCACTGGCATCTCTGTTGCTCTG
siSG2141 a	113 CT ...	---	

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siSG2148	50 A G ---	---	TGGAAACAACCGCTATAGTCTGAGTCATATTTTATAGACCGTGATTTCTGAGAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACITGTGATGTTCCACAGACGAGCTC ATCAC
siSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCAAGCGTTTATATGCGCAGATGAGCTGCTACAAATCTGTTGTGTGCT ICITGCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT AOCITGGGCGAGGGAAGGAGTGGAAAGGACCA
siSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTTGAGCCCTGATATTCACACTACITCTACATTTCCCTCCAGTATAATA GGAACCTCATCGCTAACTTTGAGCACTTAAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
siSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAAAGCTCCGGGCTGGTCTGTATGATGTCTGTATATTTATGTAT AATGCTTTACCTGATGATACCCAAACATATTACTAGCCTTAGATGAGGATGGATGGCAGCTGGGCTG GTCAAT
siSG2243	85 G T ---	---	CAITTTGCTCCTCTCTCCAGTACTACCCGTCAGCAACTGCTCTCGTATAAATAGTATCA GATGGTCAGTAGAAAGGIGITAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTTCAGCT TCAGTGAITTTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGCAGGCTATCAGAAAGGCGAGT CCTGTGAGGAACTCTGCGCAAGCACTGGGCTGCTCTCAGGAGAAATTTCTCCT
siSG2257	65 A C ---	---	GTCTCAGCGTAGAGGTCAGTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATTTTAC [A]GTATGCTCCCATTTGGGTTTCCAACTGATACAACCATGAGGTGAACACTTTTCTACTGTTTCACAG TTCTCCAGAGA
siSG2308	67 A G ---	---	GAAACTACCCACAGCATCATGTTTAAAGAAGAGAGATGAAAGAAAAATCCCCGCAAAAAACA AAAAATGTGCAAGTGAGGGGGCTGTGGAGGGGTGAATG
siSG2334	70 T G ---	---	AGAGCAGAAATGGTGAATCAACAAGACCTCAAAATTTGCTTGACTGCAAGAAGTAAGTGTGCTCACTTC GTCTCAGAGTCACCATTTACGGTACTGTCTATCTGGCTGTCTCTATTCATCA
siSG2339	63 T C ---	---	CAAGACTAAGAAAGCCGACCGAGTGGTCCACTCAAAAAGAGATTTCTGATTTACCTCAAAATG CAGAAACCA[CT]TACAGATTAAGAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAAGTGTGGGTATGCA
siSG2465	76 C T ---	---	TTGCAGGCTTGTATTCCACAATAACAAGTCATGTATAGAGAAATGAAATGATACITGAAACCAA GATATATAAATATTGAAGTCATTTTATGCTTTTGTAGTACTGGGTTAAATATGCAAGCAGCTAAAG GAATATTCTACACCAACCCCTTTTAACT
siSG2549	140 T C ---	---	AATTGCCAAATGGAATTTCCAGAGGATTTTACACCAACTTTGCCCTGTTGCTCCAGTTTGGT CCCAATATAGGCTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAGCA[IT]GGAACAATC CCGCCAGATTAATAT
siSG2577 b	123 T G ---	---	

stSG2577 a	121 C T	AATTGCCAAATGAAATTCOCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCCCGATTTGGT CCCAATATAGGCCCTTCGCAAGAAAGAGATCAATGCGGAACCGAACTGTGAAAG(C/T)ATGAACAATC COCGCCAGATTAAATAIT
stSG2700	58 G A	ATCTCTGACTGCTTAGTGGGAAAGGAATCAATTATTGAACCTGTCGGGCCCG(G/A)AGTCAC TCAGCGTTTGGGGAAATAAACCACTGCTCCAGAGCAGAGGAAGGCTACTTTGCAACCGGACACCA
stSG2724 b	101 T G	AAACAAGCTTTGTCAATTTTCCACTACATTTGTGTGCTTTTATAATAATTATTTGCAAACTGCTATAAT TTAATCTATATCCAAATGCTTGTCATAATCA(T/G)TTTTTTTAACTCTGGGGTGTGAAAGAAC
stSG2776 a	65 G A	TTGCGCGATCTTTACTTTCCAGAAAAGCGGTAATAAAAACCTGTAGAAAAGTCTCGAATATGCG(G/ A)TATGGCCCTTTTGGAGTTAGGCCCGAGGAATCTCAAACAAGGGACACTGCTGGCCAAACCCACAAAA ATATCCACTAATTCGGAATATAGTAACCCCTGCTTGTCCGGAATG
stSG2791 b	109 G T	AAGGAAAGGTGGAGGGAAGGAAGGAAGAAATTCACATGGTTAGAAAAAGACCACTAAAGATTATTTTC TATTACTTCTGAAACGGTAAACTAGCAATTTTATAATAATT(G/T)GGGTCCTCAATTAATCTATTTA AAGCAGAAAGTGTAAAGCTATCTCCATTTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G	AAGGAAAGGTGGAGGGAAGGAAGAAATTCACATGGTTAGAAAAAGACCACTAAAGATTATTTTC TATTACTTCTGAAACGGTAAACTAGCAATTTT(A/G)TAAATAATTGGGTCCACTTAAATCTATTTA AAGCAGAAAGTGTAAAGCTATCTCCATTTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85 C T	CCGCAATTTTCAACACACATCTATGAAAACTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAA(C/T)GAACAAAAATAAGAAAGAAAAACCCATGAAATGSCCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A	ATGGGTGCATTGTAAGGCAAAATTAATACTTTTTCAGCGAGGGGTGGCAAAATTTAATGAGCTGA TGTGTCCCAAGGAGACGGCG(G/A)GGCTCACACATCCCATCAAACTACTCCTCCCAT
stSG3031	71 T C	ATACTACAGGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCTCAAGTCTGGCATTTTCTGTGGTGTGTCAGC AAAT(C/G)GCCCTTTATTTTAAATGATTCCAGACATCTCGGCAGCATAGCT
stSG3058	81 G A	GTCCCAACTCCTCTCTCTTAGAGAAAAACTGATTAACCTCACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC(G/A)TGAAGAAGCATCAAGGCCAAAAAGGCAAAACTGGCTGAGGC
stSG3092	94 T G	CAGCATCTCCAGAACATCTCTAGAAGTGAACCATTTCTGCACTATTGAAAAACAAGCCCAAGTTTC CAAAATCCAAAAATAATAATGAACGTGCT(G/G)GATAAACATCTCTTATGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G	AAGAAGTACTTTTGGTACGTATTAAATAAGAGGGGGTGGGAATGAATGTGAGATACAGAGCACTGTG CATCTTTTAGTCAATGTACGTGGAGTGA(G/G)GTGGGTGCTAAGTGTCTGAAGTGAAGTAG
stSG3245	160 G C	ACATCTCATACCCAGTAGATCGAAAGGAATATCTGAGCAAGCAGCCCTGCTCCAGGGGGCC CAGGTATGTAGAGGCCCATGTGGGGTGGCCACTTGGTGTTCCTAACACCCCTGCOCATCCAGTCTG GCCOCAGTACCTACCTCGGAGGGT(G/G)CTGTACTTGGTTAAGTACTTTCATGCTTTAT

siSG3265	42 T C ...	---	AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAATGCGCAATGTGTAATGTTCTCAG TTTTATTATGGAAGATGATGATTTTCAAGCCACATTCAGTGTATGTTCTTAAATACACAATCGAC AGGACTGTCTGTTCAGTACAAATGAGGACAGCTTTTTCAGGGCAATGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAA
siSG3269	141 C T ...	---	TGTACTTACTGTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCCCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCTAATAA GCATGAIC/TJGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3269	24 A G ...	---	TGTACTTACTGTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCTAATAA AAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3284	130 C T ...	---	TTAACTCAAGAACTTTTCAAGTACAGGAAGTTTATCTAATTTAAATGACTAAATTACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCA/C/TJ TCCCTAACTTTTGTAAITGCTGTAAATGGGACATTTGTGTTGATCTACCC
siSG3292	99 A T ...	---	GTCTCAAGTGAATCTGTAATACATTTTAACTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/JTJACAAATCAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGCTCTCACTC/AJCCAGTGTATCCATTTTCCCGAGCGGTAGAGCTTTTCTG TTTCTGTAGATTTGCTGTCTGCTGACATTTGATATAATGAGTGTGCTGTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCACTTCTTCTTCTTAA
siSG3323	26 C A ...	---	GATCCCGAGTATTATTTCTAAATTTGAACCTTTGTTGTGGAATAAAAAATCTGAGGACCCTCAGAG GG/CJATAAGGGAACCCCTTTTGTCTTAGTTCTATAAGGACTTTCT
siSG3369	69 C T ...	---	CAAGACTGTAGAAGCTAGGCTGTGTAGAGTGAAGGAGGATGCTCGAATTCGCCAGGACTCAGG CTCAGCTTCACAAATCCGAGGAAAGGAATGACATTTCCAAACTGTCACTTGTAGCG/GTCTGGGT CAAAGTCTAAGAGAGCAATAAATAGAGACT
siSG3398	125 G T ...	---	TCCTTACTGTTAACCTGAGTCTGGAGTAAAGGATGCAATCACG/JGJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTATCCTTCCACCTCAGCCAAGTGTAGTGGCTGACAGGACAAGTCAACCATGCTA CCTAAGTTTGTAGAGACAG
siSG3416	43 A G ...	---	GTAAGACAAAGTTTTCGTATGTTGACAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCTCCCAAGTCTGTATTTACAGGTGTAGCCACTGCCCGCCCGCTTTTAAACTGAAT GTTGAAAAATCATCTGCTCTTGTCTGGTAACTGAT/JCAAGTGTGCTTAACTTGTGTAACCCAC TTTCCCTTATCTGTAACAAAATGGACAAACAGAACTTTTCCCTTCTCTC
siSG3424	173 T A ...	---	GTTTCATGTTAAGATTAGGAAGCTGTGGATGTGAGGGGTCAAGTGTGATGAGGGCCTCACAGA ATGAGTGGCAGAGAGGGGCCCT/JA/GAAATAGCTTACTCTGTGTTTCTCTATC
siSG3436	88 T A ...	---	

siSG3483	103 C T	---	---	GATACAGAAGATAGTGGTATGGATGGATAGTGAAGGACAAATAATACAAATATATTTTATTTG AAATAACAAAAATGCATACACAGCTCAATGGGTGAC[C/T]TGGAAACAACTTGCTTGACTATATTA CTGA
siSG3491 b	71 G A	---	---	CAAGTACTCTATTGCTCTAAGTAGTGCAGTCTGGCAAATATTTCTCAGCAACAGGACGATTG AAG[A/G]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCTGCAATTTAGCAGTCTGA ACAATCTTTCTAATCTTTTACTGGCACCTGTGGATTTCTATTAACCTCATTTACTATTTTCTGTGATG ACAGAAATAAGTTAAC
siSG3523	33 C T	---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]TJGCATATATGTGTACAAACACACACACACC CCTAATTCCTCAAAATGCTCTGGCATAAGTTTATCTTACTGGTCTG
siSG3536	213 A G	---	---	AGTACAAACACAGATTTAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATAGTGGCTTGGTGAACGCATCTCAGTCTCATTTCTTATTTTATTTTAAATGAGCTTG TGCACCATTAG[A/G]TCTGCTGGGTGTTCTCAGTCTTGCATGAAGTATG
siSG3583	112 G A	---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACCTAC
siSG3586 a	60 G C	---	---	CCTAGTAACATAGTGAGACCTGCTCTACTAAAAATTTAAAAATTCAGGTGGTGGTG[C/C]ACG CCTGTAGTCCCTACTTTGGAGGCTGGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101 T C	---	---	ATATAGTCTGGTAGCATATAAATCCTTTAAAAAGCAATCTGGCCATATCAAGGCCAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGAT[C/C]CTATTTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAAAAAGCTATATACAC
siSG3590 a	70 A T	---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTTCTAAAAA AAA[A/T]TTTCTGATGCTCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
siSG3619	78 A C	---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGGAGCTTAAATTTCTTGAATTCATACGGCT TCTGTCATT[C/C]AACAACTTCCAGAGAAAACTGGGCTCTATATTTAAG
siSG3644	40 T C	---	---	ACATATGAATGAGCTTATAGTGGCATATTTAGGATGAGAT[C/G]GATTGAGAGGATGAACCAAGG ATGCGTAATAATCAATTATGAATAAAGTTATCTGGGGAACGGCCATTTGTCCAAACATTTACTAA GTGCTACTA
siSG3646 c	70 G A	---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGAACAAATAATATGCTTACT GGT[G/A]ATATTAAGCTTTGATACCTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTTGAGATCAIT CTTCTTTTGA

siSG3646 b	55	A G	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAJAGJTATGTCTT ACTGGTGATATTAACTTTTGATACCTTGGTTAAGATGGTGTCTGCTAATTTTCCATTTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43	A T	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAATATGTCTT ACTGGTGATATTAACTTTTGATACCTTGGTTAAGATGGTGTCTGCTAATTTTCCATTTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85	A C	ATTGTTCCCTGAACATTCOCGTGGTCTCCTCTGAAAGCCGATGACCATCCAAOCCTGGACTACCT GAAATATCCTACGAGGGCAGCTGGCCCTCCGAGACTGACGATTATTAACCCACACACGGAAGG
siSG3693 a	30	C T	ATTGTTCCCTGAACATTCOCGTGGTCTCCTCTGAAAGCCGATGACCATCCAAOCCTGGACTCA CCTGAAATATCCTACGAGGGCAGCTGGCCCTCCGAGACTGACGATTATTAACCCACACACGGAAGG
siSG3698 b	145	G A	TCTTGCCCTTTTGTTACCCCTAGAGAGATGGCAOCCAAATCCCGAGGGTCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG(G/A)GAATACCCACCCACCTTCCCTCAGTGCAGA
siSG3698 a	51	C G	TCTTGCCCTTTTGTTACCCCTAGAGAGATGGCAOCCAAATCCCGAGGGTCTCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCCACCCACCTTCCCTCAGTGCAGA
siSG3724	107	C T	ACCAGCCTCATGTGTCAGAGGGGTCTCCTGCTGATCCCACTGGAGGCCATCCCTGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTCTCAGTGTGAAG(C/T)ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTCT
siSG3725	104	G A	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCAGCTCAACAGCATTTAA ATCAATAATATTATTACAGCCCAACAGCAACAGCC(C/G)AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
siSG3751	128	G A	CGGAAGAAAGAAACAAATCCACAGGAACAATCTATGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTAAAGGGGGAAGCAGGCTGGAGGGGAAAGAGAGAGATATGGTCC(C/G)ATT GCTGACTCCTATGTTGCAAGAG
siSG3787	49	T A	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTTATTAJAAAGTCCCTAAGA CACTGAGGGGCAATAAACCAACAAAATAAATAAAGGAGTGATAGGCTAAAGAGATATCTTCCCT GACAGAGGAAGAGATGGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGGC CACCACACCTCTGTGGTCAAGGGCCCTCTCTGGGAGCAGGCTAG(C/G)GGCAGGGAGGATGCAG GGCTGGAGGGGACCCCACTGGGGACCCCAAGGAGTCCATTTCTGCOCT
siSG3880 b	115	G C	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTTATTAJAAAGTCCCTAAGA CACTGAGGGGCAATAAACCAACAAAATAAATAAAGGAGTGATAGGCTAAAGAGATATCTTCCCT GACAGAGGAAGAGATGGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGGC CACCACACCTCTGTGGTCAAGGGCCCTCTCTGGGAGCAGGCTAG(C/G)GGCAGGGAGGATGCAG GGCTGGAGGGGACCCCACTGGGGACCCCAAGGAGTCCATTTCTGCOCT

siSG3880 a	36	G C	---			GACAAGAGGAGAGATGCGCCAGAGACAGGGCTG/CJGAGCTGGGGTCCCTGAGTGCCAGG CGCCACACACGTCCTGTGGGTCAAGGCCCCCTCTCTGGGAGCAGGCTTAGGGACGGAGATGCAG GGCTGGGAGGGAGCCCACTGGGGACCCAAAAGSAGTCCATTCTGCCCT
siSG3895	44	A G	---			AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTGTA/GJTITTTTTTCCATTAACATAA TACATGCCCTCATAGATATATCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAA
siSG3902	104	T C	---			TCTGTGAGACTGGAGAGACAGGTACCAAGCAGGCTCTGGTGGGAACCTGGCTTCTGATAACA TCATCTATTTCACCTAAATGTGAAGCTGCTTCTTTTC/JCJGAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTGTGACAAT
siSG3935	50	G A	---			GGGTGTCTGAGGAGGACAGGCCACCCAGGATTTCAACAAGCAATTTGTCQ/GJCTAGTGTGCAGGC TCCTCCCCAGTTCCACAGGCTGAGTACTATGGGTCAACAACCTTCTGGAGCT
siSG40	25	A G	---			GAGGAAGAGGTTGAAGAAGTGTGA/GJAAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGTGTGATGCCCTTACTATTAGATAAGGAACAAAATAAACCTTGTGTATGTATCA CCCCA
siSG4009	32	A G	---			GTGTGGCTGTCTGATGATGAATGGCGCTCJAGTACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCACACTGCTTACA
siSG4033	123	T C	---			AGAAGCCTTGGGACAAATGGCAGTGGCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTTAATGTTTCAAGCATAAAGGTACTTTT/CJGTGAAC AGTGGGCAACAC
siSG4038 a	29	G A	---			GCTGAGACAGTGTACAGCCAGCCCTGTG/JCGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACTGAGGGTTCATCACT
siSG406	53	T C	---			ACTGTGTTCAACAGTATTGCGTTGTGACAGTAGGAAGCTAAACGAACAAAT/CJGGTTTAGTT TTGCTGAAGACTGGCTTATTAATGGACAGCTTTCTTAACAAGAGATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T	---			ATCTGGCTGAATTAGTCAAGCAGGTCAAGATACTATTGTCTGATGATGATTAG/GJTAAAAAA GTTTGCTGTGTAATCTTTAAAGCTTGCTTATCTCATCTGTAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCAATGGCCTTCATCCTGG
siSG4095 a	27	A C	---			ATCTGGCTGAATTAGTCAAGCAGGTCAAGATACTATTGTCTGATGATGATTAGGATAAAAA GTTTGCTGTGTAATCTTTAAAGCTTGCTTATCTCATCTGTAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCAATGGCCTTCATCCTGG
siSG4120	65	G A	---			TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATAC(G/ A)CTTTTCCCTCAGAGAGCCACAGTTAAACAGTTCCAGCACACCATTAATCCACCGAGCT

siSG4128	54	A G	---			CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCTCTTGTGTACATTCTTJ/GTATATTAATTT TACTTCTTCTGAAATGCCCACATAATTTTGAATAATGATTCACTCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCCAAATGTTCCAGAGGG
siSG4209	128	G A	---			CACGAAACAGATGAGCCTACACAGTGTCTGTAGGACCGAGGCTCACAAACATCCACATGCGACAAGC AGGGCCGCGCCACTCCAGGCAACAGAGCCACCCCGAACCCTTGCAGAGCGCGCAGCTCCCTCTG/AGC AGGGGACCCAGCGAGCGACAGGTCTTTTGTATGCTCCGAAAGCTGAGCTCCATTCCA
siSG4209	65	G A	---			CACGAAACAGATGAGCCTACACAGTGTCTGTAGGACCGAGGCTCACAAACATCCACATGCGACAAG /ACAGGGCCGCGCCACTCCAGGCAACAGAGCCACCCCGAACCCTTGCAGAGCGCGCAGCTCCCTCTG/AGC AGGGGACCCAGCGAGCGACAGGTCTTTTGTATGCTCCGAAAGCTGAGCTCCATTCCA
siSG4254	31	G A	---			CAITACCCAGAACGCCATGGAGGACAGAGCG/AGCAGCGCGCGGAGCTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGCGGGGCTGCTCCCGGAGCGAGCGAGCTGAC TGGGGGACCCATGGCGGAGAGAGGATGACCGGGTCTATG
siSG4301	81	T G	---			TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACACTTTCCAT TTAAGCAAAATAAATJTG/AGCTTCTGTAGTAGTTGTCCCGAGTTTCAACCAACATTTTG
siSG4331	71	T G	---			CTCACAAAGGCCAACACAGAAAGATACAAATACATTTCACAGCTAATATTTAGTTTTATGACAC AGAGTGTGTTTCAACAAGTTTAAAGTGTACCTGAGAGCATGTTAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCCTCGCCCTTGTGATCTGTGAGGGGTGTGC
siSG4340	76	G A	---			TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTATGATACAGAAAGTCAAAACCC ACATGTTCTG/ATTAAGTGGGAGATAAACAATGTGTACACCTGGAGCTGGAGAGCAGAA
siSG4361	109	A C	---			TTCCCAACCATGAGTGACAGAGCT/PCAGTCAATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCAACAAGTAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGAGG
siSG4361	24	T C	---			TTTCACTGCTACTGTGGTGTCTGAGTCTCTCAAACTGCTTTTSCAAGTGTCTTCCAAAGGGGAG AACAGTGTGGAAGTGTGGCTCTGCAAGAAAGCCATCTTTCCAAAGGCCATTTCTTCTCAGCTGC
siSG4376	73	A G	---			GAAGGCCACAACAACACTCCTAGCCAGAGAATGACAAACATACGATTTTCTT/CTGAGCTGTGTAGT ATCCACAGTAGTGTCTGTGTCATGTACAAAGTGTCTGCCAGAACCCCATTAATTCATGCGC
siSG4381	50	T C	---			ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCGAG/AGTGCACACGAAACCCAGTGGACTGTGAAACTCAGGCTGCAGAGGGGTGGCTTGT CAGCTGGGT
siSG4410	79	A G	---			

siSG443	65	C T	---			AGCAGATCAGTCCGACCTTGTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C
siSG4430					---	TGATGCAATGAGAAATAACCAACTGGTAGGGGAGGGGAGGGGAGGGAATAGGCAC
a	54	A G	---			AAATGGAATTCATCTGGCTGCTCTCTCAGGTC
siSG4448	99	G A	---			ATGCACATTAAATGAATGGCCTAACTACTGGAACTTTAGTAGTTCTATAAGGTAGJATTAACATA
					---	GGTAGGATCCAGTTCCTATGACAGGCTCTGAGGACAGATAGAGGCATCAAGAGGGCCATTTT
						CCTCCCTCCCTTCCCTTCCCTCCAGTCTTCCATACTGTCCCTCCCTCCCTCCCTCCCTCCCTCCCT
					---	CGCCTAGCCCTGCCCTCTGGGGTCACTGCG/ATGGGTAGGGCCCCCAAAAA
siSG4449	92	T C	---			ATTAGCCATTTCATCTTGCACAAATTTGCTTACTGTAACAAAGTACTGTACTGATGATGTTTACAAT
					---	TAACITTTGGACAACCTTAAACTTAT/CJTAGTGACATTGCTCTAATAATCAAAATACITCATCATA
						GGCTGAACATAATTAATAAAGAGCAAAAGTTACCCCTCC
						CAGACATGAGGGATGGCCCTGTCTCTCTGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
siSG4467	42	C A	---			GAATGAACTCAAACTCTTCAGTTTTCAGTCACTTTCTGGTATCGAGCCGACACACCGAGGAG
					---	CACACCTGCTTCCAAAGGCTGCTGCTCTCTGCACACAGT
siSG4475	21	A C	---			ACATGTCTTCTGACCAAGCA/CJATTAATAAGTTTATTAGAAAGAAATGAGTTGAAGTGAGCGA
					---	TTAAGAGACACAACCTGGACTTTTGTCTTTCTTACTGTAGCACCAGGTTTCATG
						GTAACATCTGGGGTGGGGTGAGACAAACA/CJATGAACCAATAATTAATTAACAATTATACATT
						TCAAGGAGACTTTTAATCTAGGTTAATGTGAACCGCAGCCCATCAATGGTTTGTTCAGGAAAAGGGAGA
siSG4477	32	A G	---			TGAAGTCTTGTCTGGGCAAGTTTGGCTCATTCGACGTGAGCTTGGC
						TGAACCTAGAGCTGGGTGGGAGCTGCAGGAGGGAGGCTGGGGGCGCAGATGAGCGCGGGGGA
						CAGCAGCGTCC/CJTGCCACGCTGCTGGCTTGTAGAAAGAGACATAGGCTGCTTGGACTCGATCT
					---	GATTCCTATTGACAGGGAGACGCTGTGTGTCATCA
siSG4531	79	C T	---			TGCAATTAAGGAATGATACGGCATAATTGGGGGACAGAGAACAGGCTTGTATGAGGACAGAGTCTATT
b	86	G A	---			AAAAGAGACAGTGGGCAC/CJACAATTGGAGGGGAAGCGGGGAGGGTTTATAGAAC
siSG4550						TGCATTAAAGGAATGATACGGCATAATTGGGGGACAGAGAACAGGCTTGTATGAGGACAGAGTCTATT
a	85	C G	---			AAAAGAGACAGTGGGCAC/CJGCAATTGGAGGGGAAGCGGGGAGGGTTTATAGAAC
						AATCAGGCACAAGCTCGGAGAGAGCAACAAAGCTTCTGCA/CJATGGGAGGGAGACAC
siSG4590	47	A G	---			CATTGAAAAGGATCGTCTCTCTCATGCAAGCGAGGCTGCTCCACAGGCTGCTCTCTG
						AACTGTATACCCAGCGGTG/CJCAATGACTAGTCTTCCACAGGGATTTTATATACTATTC
						CTATAAGGTTTATCATGAATAAAAAGCTCAAACTCTTTTCAGCCATTGCAGATTCACATTTATCT
					---	TAATATCTGTTCAAGATGCTCTGGAG
siSG4623	22	T C	---			TAAAAAACAACCCCCCAAAAAACACCCAGAGTTTGTAGTTTATGTTTTCAGATTAAAG
						GTATTTCTTCTTAGCTTCTAAATTTTGTAGTCAT/CJATCAGAAAGTCTTCCCTACTCCAAAGTGA
siSG4843	102	A C	---			GAAAGGA

[illegible]

ESTD-C7	---	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	---	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAAATGGGAGTGGCCAAOCATAGGGGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGCTTCTATTATGCTCTTTCCCGGCTCTCTCTCACACAC
ESTD-CB23	---	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCGGGCTTCTCTCTCACACATACACAGAGCCCTACAGGACGAGAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTTTCCACCCGA GGTGGCTGTTTGGGCCATCAAGAGCAGAGATCTCCACACCCAAA
ESTD-CB24	---	---	---	---	ACCAGGACCAAGAGCTCTCAGAGCAACCTAGCCCATTAACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCAGGCTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAG GCCACACTGATGCTGGCCAGCCTTCTACCCGACCCAGCTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGTGACAGTGGGTCAGCAGACAGCCGAGCCCTCAAGGAG
ESTD-CB25	---	---	---	---	GTTCCTTTCAGAGTGTGGCTCACTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTTCGCGCTC TCTGCTCTGAAACCAGGGCATGGGAATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTTGTCAACAGAGTCTTACCAGCAAGGGTCTCTCTGCGCAAC ATCCTCTATGAGATCTTCTAGGGAAGGCCACCTGTATGCGGTG
ESTD-CB27	---	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCCTGGTTGCATTTCAGGAGTGTCTGTGGAGTCTGCTCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCTGCT TTCTCTGTTTCATCCTGATGGAAGTCTCTCAACACCCATTTCCATAAC
ESTD-COL2A1c	---	---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTGCTGACTTTCAGGGTGTCAAGGTGGAAAGGT GAACAGGGTCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCTCTTG GTGAGCTATTGAGCTGTAATCACCATACCTGACCT
ESTD-COL2A1d	---	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGAACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACTGGACCTTCTTCTACTGACGACAGAACTTACCC AAGAGAGATTAAAGGCAAGATACAAATACAAATTTTATTTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	---	---	---	---	GGCCAAATGCCGGGAGTTTCTCAATGTGTGGAGAGGCTTGAAGACATGTTTGTGCTTAGAA GGCAAAATCCATCAAAAGTTAACTTCTGGGCAAGATGAAGAGCTACCATCACTTCTCTCATGAAAC TGGGAGGCGCGCATAGTCTCATGCTGTAATGCCAGCATTTTGAAGAGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAAGCAACCTGGCCAAAT

ESTD- G00H	..	--	---	---	---	CGCAGACGGTCACTAGTGGGGTGGGAGTGTGAGGGGAGGAGGAACTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTCTTGAGAGAAAGCGGAGAGACACAGACCACTGGCTAA GTGTAAGGAGACCTCTGGTGGCAACGCTGTCTGTCTGGCCCTGTTCAGCTGTCTGTCTGGCGAGTCGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	..	--	---	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCAACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGCGAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGAAATGCGAGCGGCGCTGAGCCCGAGGAGCAGGCTAGGATGTGAGAGACACAGTCAAC TGCAGCCTAAATTACTCAAAGCTGTCCCGAGGTCACAG
ESTD- GNAT2	..	--	---	---	---	GACCCGTAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCCACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPK2L	..	--	---	---	---	AGTCTTCATCTGGGTGTCCAGGTAGATCCCTTTCAACCCCGAGAACTGCTCGATATC
ESTD- HRAS	..	--	---	---	---	CTGGCTCCCGCCAGCAGCTGCTGGCACCTTGAGCGCGCGGCCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	..	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCCAGTCTAIGTGGCAATGTGGCCTGGGCCACATTTCTGGCCCTG AGGGCCCTGCAAGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTAACCAAGCTATGATAACCTTAATTACACCCGTAGCAAGAGTTCGGCCCTCCGGCTTGATTCC AGATGGAGCTTTCTTTATCCCTGATGTATTGGATTGGCTTCCCTGCTG
ESTD-HT2	..	--	---	---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAGATGTGTTACAGTTTGTGACAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTGTGTAAGTTTCAAACAAGACACACCTT
ESTD-HT4	..	--	---	---	---	ACCAACGAGCGCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAAGTGGTCTTGGTGCCTCTATCGGCAAGATGCGTACTTATTTGAATAGTAGGTA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTCTGCGAGCGCGTGAACCCCGTAGCCTAAA TGACAGCCGAGAGCGCGAAGACATGCAATGTGTC
ESTD-HT5	..	--	---	---	---	AACACAAAGCCCGCAGCAAGATTGAACCTCGCGACCCCTGGTTTACAGACACAGTCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTCTTCTCTTCTATAGATTGATGTTATGCTCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- GFBP1	..	--	---	---	---	ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGTGGCCCTGGGAGGAAGAGAGATGTC CAGGGCACACATAGCTTAGTGAGACTC

ESTD- IGHV4-6	TTTACTATTTCAATGGATACAGAAATTGGGGAGTCACATATTCCTATGAACAAAAATTCAGATTT CAGTTTAAGTAATGTTGCTTACATTTGTGTAGTACGGGGAGTGGTGATCGGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGTATACGAACGTGAAAGT ATGTAATACTTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCAACCAATAAATGTTAGCTATTACTATCATTTATTATTATTATTATTATT AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGCACAACTCTGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCTCTGCTCAGCTCCGCTCAGCTCCGAGTAGCTGGGAATACAGGCCGCCCACT GTTCCCGGCTAATTTTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCTGTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAGGAAGAAAATGCAATTTAAAGTAACCTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAAGTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAATTGATA
ESTD- KRT8	ACCTCACCCCTCCTTAGCCGTGGGAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGACACCTTTGAGAGTCTTAACAGCAGGGCCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF78	GGGTGATTTTGAGGCTCAGTTAATATTCAAAATTTGAACGGTAGCAAAACTGCATGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGTGTATTACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACAGGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	TACACACTTTCCTTACCCATTCTACTGAAAACGACTCGCAAACTGGAGCCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-ILPL	TGTCAGTGTCCCTAGGGGCACTCACCACCTCCAGCTCTCCCTAGCCGAACTTCAGCAACGTCAG AGGGTTTGTCTAATCTCAATCAATGCTCTTCATCTTTTAGCAGCTGTGGGGTTTTGTTGTTGTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATATAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACACATTTATAAAAATTTTTTCCACCTG
ESTD-MCC	TTGTCAGGAGTGTGCTGATGTGCTCCCAAGCTCTGCTCCCTAGCCGAACTTCAGCAACGTCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAGGAGCAAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTCCAAAGGTTTGGTCTAAGTGTGCTGATTCGCCGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCTGTTTGTAGCATGG
ESTD-NF1	ATTATCCAGATGAATTTACAAAACATATACAGATCCCAAGACTGATATGCTGGT

[illegible]

EST11458 6							CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCAGTGTCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTTCAGGACGGACCTGTCCCAAGCCAGATGATTACCATTTTCACAGTGGT CCATTAAACAATTTCTATGAGCCAGGAGAGAGATTACGTTATTCCTGCAAGCCGGCTATGTGCC CGAGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8							CGGTCTTCTCCAGGATTGTTGCAAGGCGGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTACGTTACAGAAAGGAGATGATGAACAGCA GGAACACGTGGAAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST6248 0							AOCTGGTGTGCTGTGGGTGAACCTGGTCTCTTGGCATTTGCGGCCCTCTGTGGGCCCTGTGG TCCTCTGGTGTGGTGTAGTCTGTGAGTCAACGGTGTCTCTGTAGTGAAGTGTGCTGTGATGCCAACC CTGGGAACGATGTTCCCGCAGGTGGGATGGTCAACCGGACACAGGAGAGCGCGGTTACCCCTGG CAATAT
EST38027 2							AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTTCATGCGCCTGTGGCCAACTATGCTCTCAGA ACATCACCCTACCACGTCAAGAACACAGCATTTGCATACATGATGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCAATCTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTTCACTTACACT GTTCTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAGACAA
EST12274 0							CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGTCTTCCAAATAGAGCCTTACCAAAAGTGTAT TACATAAAGAGTCAAGTGGTTTTACTCTCTCATGACCAATAATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCCGATGGGTGAGAACTGTTCTGTCCACCATGAGGATACTATAACTGTGGAAGATAA ATTCAAGCCACAGACTTGGCCAGATC
EST76807 EST44438 7							ATGCTAAGGGGATGAGACATGAAGAACCTGTGAGCCGATTTGCTATCTCCAGCGGCCCTGTGCATC CAGCTCACTCATCAATGGGGCCAGTCAAGGCCACAGGCACTGGGCTCCGGAGACTCAOCCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTTGAAGGACTTCTTG GCAAGCAGGAGGCGCTGACCCATGCCCCGATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCTT GCTCCGACCTAAGCGGACAGCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3							TGCAAAACACAAAAATCTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGATTTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGGATGATTTACTTGAAGGAACTTGAATGTTATTCAACTGG ATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATCTAGCTTAG
EST54419 8							CTTCTGCTTAATTTGAATGATTTGTTGCTGTGGGACCTGAGCACTTTTATGGACAAATGATCACTA TTTCTTGACCCCTACTTACAATCTGGGAGATGTTATTTGGGTTAGGCTGCTATGTTGCTACTA TAGTCCAAAGTGAA

EST26021 1	---	---	---	---	---	TAATGTAAGCTATCCACAAAGAGCCGTGACCATGTTTGTGAGGTTGAGTGACATGTTGGAACCTGT CCATAAAGTAATTTGTGAAGAGAGGAGCAACATTCCTCTGCAGCATTCTCTGCAGCATTCTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGAGAAATGCATTATGTGCACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGTCAACAGACAAAGCAAGCC
EST51212 0	---	---	---	---	---	ATCCTGAGCTCGCCCAATAAGCTTTCTTGGTTCTACTTCTCTCCACAAGCCCCAAATTCACTTTCTCA GAGGAATCCCAAGCTTAGAGCCCTGAGCCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	---	---	---	---	---	GTTCGAAATCCTCCTCTGAAAGTGGCCGGTTTAAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTTGAAGCTGGAGTGGGTTTAGGAGCGGGTCTCTGCTGTCATCTCTAAGCTCT GAGAGCAACCTCCTTGAAGCTGGGAGTGGGTTTAGGAGCGGGTCTCTGCTGTCATCTCTAAGCT CTGAGA
EST53018 8	---	---	---	---	---	ACAAATCCAGGTACACATTCAGAAAGAGGGGTGTGAGTGGCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	---	---	---	---	---	CTTCTATGGGATTTGACTTTATTTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAG GAAGCTTCAGGCTCATGACAAATTTGAAGCTGACAAATACACAAAGAGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTGAAGTTGTTTGAACITGGTGTCACTTTAATTCACACCTAG CAGACGGAACCTGAAGTCAAGGGTGAAGAAAT
EST34088 2	---	---	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAGAGAGCCGCTCAAGG ATCCCAAGGCCAACTCCCGAACCCTCAGGGTCTGTGAGACGCTCACTAGCTGCAATGGCTACA GGTAAG
EST37382 5	---	---	---	---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCTCTCTGGA CTTTGAGTCAAAATTGGCCCTGGACTTGAGTCCCTGAACCAAGCAAGAAAGAGGCCCAAGAAAT CAGAGGTGGGCACBTCCGCTCTACCCCACTCTCCCTCTCACGGGAATTTTCAGGGTAACT
EST74082 0	---	---	---	---	---	TCCAGGTGGCTGGAGCCCAAGGCCCAAGCTCTGACAGGGGAGGAGCTGGGCTCGTGAAGCATG TGGGGGTGAGGCCAGGGGCCCAAGGCCAGGGCACTGGGCTTCAAGCTGAGCCCTGAGCCCTGCTC CCAGTCACTGCTCTCTGCAATGGCCCTGTGATGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TGGGAACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGGG
EST45311 0	---	---	---	---	---	GGCCTCTCTCTTCCAAATCTGTCCTCTATAGTTTCTCTCTATTAAGTGAACATACATCTCTTTAGT GGATAGATGCAACAAACACAGCCATTATGGGAAGGATCCACGTGTGTGGCCATTTGTAACA CATTTTCTGAAATCACCTCTTTTCATTAAACAGCCCTTATCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT

EST65258 8						TGCCCATCAGCGGCGGAGACATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAACCGAAAT COAGTTATTTTCCACCCCTCAAAATGACAGCCATGGCGCGGGCTCTTCTGGGGCTCGTGGGGGG ACAGCTCCACTCTGACTGGCAGACTCTTGCATGGAGACTTGGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGGGTGTTTCTGTCAGTCAAGTCAATCATGCTGATTAAT
EST38216 3						ATGCGAGGATGAAGGTGGACAGGAGGAGGCGCAACCTGTCATCCAGGGCTGCGAGATGTCGCTG GACTATGGGTTTGTACCCCACTGACCTCCATGACATCAGGG
						ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTTGTAGCATACCTAA TTTTTCTGCTCCATGAGAGTGTAGCTTTTACCTTAATGCTTTTAAATGAGAGTGAAG TTTTTTTCTGAGAGTGGCAGATTTCCAGAGTTTGTGTTTGTGAATAGCAATGCCTGTGAATAA GAACTGAATACCTAAGATTCTGCTGGGGTTTTGGTGATGCA
EST62782 9						GAGATCGGTGTGAGTTATTAGGCATGTTACCTGTAATCTCCCAATCTTGTGGTTCACCGATG GAATCGCGCAATCTCTGACACGTGTCACCCAGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCCTGGAAGACAGCAGCGGGATGGGCGCAGGAGAGCTGCCCTGGATGAA GGAAGAGATTAAAGAGCTTGATTGGACAAATCTGGTTCTTGGAGTGGAGAGTTTCATGTCTCT GCCTGAGTTACACAGAAATCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTT
EST54045 6						GGAATATTAATAATTTTAAATACCTCCATTTGCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTCTTACAAAATCGGATGGAAATCT GTTAAGTAGTACTGTTTGCCTTGGAAATGGATTTTAAATGACCTTATCAT
EST52908 0						ATCACAGTCTCTGGTCTCTGGCCATCTTCTTGGAGAGATGGATGGTGGTCTGCAAGGCCCTTTGG CAATGTGAGATTGATG
EST19590 6						AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATAATGAC
EST76136 0						TGAAGCTTCTGCCAGCTTGCAATTTCTAGGAGAACCCTGTCATACCTTTATCTATAGCTTCCCC TAGGTCTT
EST58607 0						CTCTGGATGGTTACAGGTGGCAGGACAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCTACTGAGAACAGGACAGCCACATGGCGGGGATGGCGGGGAGTCTGGT TGGCGCACCGCTGTGGCTCTGTTGTAACGAGTGGCTTTGGGTTGGATGCCCTAAACCTTTGTTCT TGGCCAGGAGGGGGGGTGGCTGCTGAGATGTAGATGGCGGC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
6=SNP Reverse Primer 7=Sequence

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.